OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 01:05:24 ; Search time 4686 Seconds
(without alignments)
10423.145 Million cell updates/sec

Title: US-10-019-337E-7
Perfect score: 1008
Sequence: 1 ctggtaagcttaaggcaga..........aactcccttgccctcaggtc 1008
Scoring table: IDENTITY_NUC
Searched: Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 9416466

Searched: 4708233 seqs, 2422767955 residues

Database :   GenEmbl1:*

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 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
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10: gb_ro:*
11: gb_sts:*
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13: gb_un:*
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	DB ID	Description
1	1008	100.0	1008	6	AX068325	AX068325 Sequence
2	1008	100.0	1008	10	RN0294476	AJ294476 Rattus no
3	872	86.5	953	9	AX068324	AX068324 Sequence
4	872	86.5	953	10	MMU276872	MMU276872 Rattus no
5	666.2	66.1	909	10	RN0294475	AJ294475 Rattus no
6	630.6	62.6	882	10	MMU276516	MMU276516 Mus muscu
7	593.8	58.9	810	10	MMU276871	AJ276871 Mus muscu
8	591.8	58.7	834	6	AX090389	AJ276514 Mus muscu
9	558.2	55.4	783	6	AX090389	AX090389 Sequence
10	558.2	55.4	783	10	MMU276870	AX090395 Sequence
11	510.6	50.7	795	6	AX090391	AJ276870 Mus muscu
12	454.4	45.1	2522	6	AX068323	AX090391 Sequence
13	454.4	45.1	245589	2	AC094932	AX068323 Sequence
14	430.6	42.7	1427	9	AF253318	AC094932 Rattus no
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16	427.4	42.4	849	6	AX090393	AJ291673 Homo sapi
17	356.8	35.4	15914	6	AX090388	AX090393 Sequence
18	356.8	35.4	47887	10	AF155960	AX090388 Sequence
19	356.8	35.4	189283	10	AL833771	AF155960 Mus muscu
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22	320.8	31.8	900	9	HSA291674	AJ276515 Mus muscu
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ALIGNMENTS

RESULT 1
AX068325
LOCUS   AX068325   1008 bp   DNA   linear   PAT 25-JAN-2001
DEFINITION   Sequence 7 from Patent WO0102557.
ACCESSION   AX068325
VERSION   AX068325.1   GI:12578508
KEYWORDS   .
SOURCE   Rattus rattus (black rat)
ORGANISM   Rattus rattus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
    Rattus.
REFERENCE   1   1008
AUTHORS   Masure,S.L., Cik,M. and Hoefnagel,E.W.
TITLE   Neurotrophic factor receptor gfr-alpha-4
JOURNAL   Patent: WO 0102557-A 7 11-JAN-2001;
    JANSSEN PHARMACEUTICA N.V. (BE)
FEATURES   Location/Qualifiers
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ORIGIN

Query Match   100.0%;   Score 1008;   DB 6;   Length 1008;
Best Local Similarity   100.0%;
Matches 1008;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Left column — alignment

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Qy   841 GAGGCAGAAACGGTCCCCGGTTTGGTGTCCCAAGGGTGTCCTGCCAATGCCCCT 900
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Query Match   100.0%; Score 1008; DB 10; Length 1008;
Best Local Similarity   100.0%;
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     1 CTGGTPAAGCTTTAAGGCAGAGGAGGACCTAAGAGAGTGAGACAGAGAGTGAGGTGAGGCG 60
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RESULT 3

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LOCUS       AX068324                 953 bp    DNA        linear   PAT 25-JAN-2001
DEFINITION  Sequence 6 from Patent WO0102557.
ACCESSION   AX068324
VERSION     AX068324.1  GI:12578507
KEYWORDS    .
SOURCE      Rattus rattus
  ORGANISM  Rattus rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Masure,S.L., Cik,M. and Hoefnagel,E.W.
  TITLE     Neurotrophic factor receptor gfr-alpha-4
  JOURNAL   Patent: WO 0102557-A 6 11-JAN-2001;
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RESULT 4

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LOCUS       RNO294475               953 bp    mRNA       linear   ROD 13-DEC-2000
DEFINITION  Rattus norvegicus mRNA for neurotrophic factor receptor splice
            variant A (Gfra4 gene).
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ACCESSION   AJ294475
VERSION     AJ294475.1  GI:11191814
KEYWORDS    alternative splicing; Gfra4 gene; GPI-linked isoform; neurotrophic
            factor receptor; polymorphism; variant A.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Masure,S., Cik,M., Hoefnagel,E., Nosrat,C.A., Van der Linden,I.,
            Scott,R., Van Gompel,P., Lesage,A.S.J., Verhasselt,P., Ibanez,C.F.
            and Gordon,R.D.
  TITLE     Mammalian GFRalpha -4, a divergent member of the GFRalpha family of
            coreceptors for glial cell line-derived neurotrophic factor family
            ligands, is a receptor for the neurotrophic factor persephin
  JOURNAL   J. Biol. Chem. 275 (50), 39427-39434 (2000)
  MEDLINE   20564314
   PUBMED   10958791
REFERENCE   2  (bases 1 to 953)
  AUTHORS   Masure,S.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-2000) Masure S.L., Biotechnology &
            High-Throughput Screening, Janssen Research Foundation,
            Turnhoutseweg 30, B-2340 Beerse, BELGIUM
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Query Match             86.5%;  Score 872;  DB 10;  Length 953;
Best Local Similarity   93.6%;
Matches  943;  Conservative   0;  Mismatches   7.5e-138;
                                             Pred. No. 7.5e-138;
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Db        802 ------------TGCTGTTTCCTGTGGGGTGGGTGTTCCTCGGATGTCCATACTCACTCACTGCCCT 845
Qy        901 GGCTCTTCCAGGCCCTGCTCTAATTAGGAAGGCCATGGACACACACACAGCTGACTGCCA 960
              ||||||||||||||||||||||||||||||||||||||||||||
Db        846 GGCTCTTCCAGGCCCTGCTCTAATTAGGAAGGCCATGGACACACACACAGCTGACTGCCA 905
Qy        961 TGTCTCTGGATTATGCTCACTGAACTGAAGAAACTCCCTTGCCCTCAGGTC 1008
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Db        906 TGTCTCTGGATTATGCTCACTGAACTGAAGAAACTCCCTTGCCCTCAGGTC 953

RESULT 5
MMU276516
LOCUS       MMU276516                909 bp    mRNA    linear   ROD 02-FEB-2001
DEFINITION  Mus musculus mRNA for putative GDNF family receptor alpha 4,
            transmembrane isoform (Gfra4 gene).
ACCESSION   AJ276516
VERSION     AJ276516.1  GI:7688060
KEYWORDS    GDNF family receptor alpha 4; Gfra4 gene; transmembrane isoform.
SOURCE      Mus musculus (house mouse)
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ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1  (bases 1 to 909)
  AUTHORS   Lindahl,M., Timmusk,T., Rossi,J., Saarma,M. and Airaksinen,M.S.
  TITLE     Expression and alternative splicing of mouse Gfra4 suggest roles in
            endocrine cell development
  JOURNAL   Mol. Cell. Neurosci. 15 (6), 522-533 (2000)
  MEDLINE   20319126
   PUBMED   10860579
REFERENCE 2  (bases 1 to 909)
  AUTHORS   Airaksinen,M.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-MAR-2000) Airaksinen M.S., Program in Molecular
            Neurobiology, Institute of Biotechnology, P.O. Box 56 (Viikinkaari
            9), 00014 University of Helsinki, FINLAND
FEATURES             Location/Qualifiers
     source          1..909
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                     /tissue_type="thyroid"
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     CDS             1..909
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                     transmembrane isoform"
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                     /db_xref="UniProt/Swiss-Prot:Q9JJT2"
                     /translation="MLRRAHLMDERPGQAIFLGLGSQRSASFTDGNRCVDAAEACTA
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                     GSRDRCPEGGPRCLRVYAGLIGTVVTPNYLDNVSARVAPWCCGCAASGNRRECEAFR
                     KLFTRNCPGSGAIQAFDSLQPSVLQDQTPAGCCFPRARHEWPEKSWRQKOSLFCPNAQG
                     VLAVCTHCPGSGPGPALIRNMNRGHHS"

ORIGIN
Query Match    66.1%;  Score  666.2;  DB 10;  Length 909;
Best Local Similarity   86.3%;  Pred. No. 4.9e-103;
Matches   781;  Conservative  0;  Mismatches  98;  Indels  26;  Gaps  3;

Qy    66 ACGGGTGCTGAATGAGAGGGCAGGCCCAGGCCAGGCAGTTTTATGGAGTCTTGGAATGCCAGAGAGG 125
Db    15 ACATTTGATGGATGAGAGGGCCAGGTCAGGAGGGATTTTCCTGGGTCTGGGAAGCCAGAGAGG 74
Qy   126 GTCAGGGAGCTCCACTGAGGGGGAAGCAGCGAGGCGTTGCACAGCAGA 185
Db    75 GTCTCGGAGCTTTACCGACGGGAATCGCTCCGTGGTTACGACAGCAGA 134
Qy   186 CGAGCAGTGCCAGCAGCTGCGCCTCCGAGTACGTTGGCGCAAGTGCTGGGCGCCGGGC------ 239
Db   135 CGAGCGGGGTTGCCCAGCAGCTGCGCCTCTGAGTACGTAGCCCACGCCACCCGGGCCCAGCGCC 194
Qy   240 ---GGGCTGGCGGGGGGACCCGGGAGCTGCGTGCGCTCCCGGTGCCCTGCCTTCGGCGCCG 296
Db   195 CGGGCAGGCCAGCCGCACCCGGGCGTGCGTCTCCGGCGCCGCCCGAGCCCTGCCCG 254
Qy   297 CTTCCTTCGCGCCCGCGGCCGGCCCTCGGCGGGCCTCACGCCACACGCCCATCGGAATGCGAAGG 356
Db   255 CTTCTTCGCGCCGCTGGGCCTCCCGGCGGCGCCTCACGGCTTCTTCTGCGGCTGCAAGG 314
Qy   357 CCCCGCCGTGGCGGCCGAGGGCCGGCAGCAGACATTCGCGCCGGTTCTCCGGCCC 416
Db   315 CTCCGCCGTGGCGGCCGAGCGGCGGCCCAGA.CTTTGCGCCGGTTCTCCGGCCC 374
Qy   417 CCAGCTGGCCGCCACCTTCTCCTGCGCTGCGAGCGAGAGACGCCGCGGGTG 476
Db   375 GGGGGTTGGGTGCCGGCCTCTTCTTGCCTCGGAGCCCTGAGCGCGCTGCGGAGCGGCAGCGCGCTGTG 434
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RESULT 6
LOCUS       MMU276871
DEFINITION  Mus musculus mRNA for GDNF family receptor alpha 4, putative
            transmembrane-anchored isoform (Gfra4 gene).
ACCESSION   AJ276871
VERSION     AJ276871.1  GI:7688068
KEYWORDS    alternative splicing; GDNF family receptor alpha 4; Gfra4 gene.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Lindahl,M., Timmusk,T., Rossi,J., Saarma,M. and Airaksinen,M.S.
  TITLE     Expression and alternative splicing of mouse Gfra4 suggest roles in
            endocrine cell development
  JOURNAL   Mol. Cell. Neurosci. 15 (6), 522-533 (2000)
  MEDLINE   20319126
   PUBMED   10860579
REFERENCE   2  (bases 1 to 882)
  AUTHORS   Airaksinen,M.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-MAR-2000) Airaksinen M.S., Program in Molecular
            Neurobiology, Institute of Biotechnology, P.O. Box 56 (Viikinkaari
            9), 00014 University of Helsinki, FINLAND
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
                     /tissue_type="thyroid"
     gene            1..882
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     CDS             1..882

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Qy   537 CTGTCCGGAGGAGAGGGGGCCGCGGGTGTCTGGGGGGCCTTGTAGGCACCGT 596
Db   495 CTGCCCCGGAGGAGGGGGGCCCCCCGGGGTCCTACGGCAGGCCTTACGACCGT 554
Qy   597 GGTCACCCCCAACTACCTGGACAACGTGAGCGCCCGAGTGGCCCCTGGA 656
Db   555 GGTCACCCCCAACTACCTGGACAACGTGAGCGCCCGAGTGGCCCCTGC 614
Qy   657 GGCCAGCGGAAACCGGCGCGGAAGAGTGCGGAAGCCTTCCGCAAGCTTCCGGCCGGCGGACC 716
Db   615 GGCCAGTGGAAAACCGGCGCGGGAAGAATGCGGAAGCCTTCCGCAAGCTTCTTTACAAGGAACC 674
Qy   717 CTGCTTGGATGGTGTCCATAACAAGCCTTTGACAGCTCGCCGCAACCATCAGTTTCTGCAGACCA 776
Db   675 CTGCTTGGATGGTGCCATACAAGCCTTTGACAGCTCGCCGCAACCATCAGTTTCTGCAGACCA 734
Qy   777 GTGGAACCCCTACCAGAATGCTGGGCGAGGGCCAAGGTGGAGGCGGCCTGAGTGGGCCTGAGAGA 836
Db   735 G-------------ACTGCTGGGGTGCTGTTTCCGGCGGGCAAGGCACGAGTGGGCCTGAGAGA 784
Qy   837 GATGGAGGCAGAAACCGGTCCCGGTTTGT------CCCAAGGTGTCCTCGAGTGTCCATA 889
Db   785 GCTGGGAGGCAGAAACAGTCCTTGTTTTGTCCTAACCGGCCCAAGGTGTCCGGTGTATGCA 844
Qy   890 CTCACTGCCCTGGCGTCTCCAGGACGCCCTTGCTCTAATTAGGAGAGGTGAACCATGGACACACA 949
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Qy   950 GCTGA 954
Db   905 GCTGA 909
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ORIGIN
      Query Match       62.6%;    Score 630.6;  DB 10;  Length 882;
      Best Local Similarity   87.0%;    Pred. No. 5.1e-97;
      Matches 737;  Conservative    0;  Mismatches  84;  Indels  26;  Gaps  3;

Qy    124  GGGTCAGCGAGCTCCACTCAG~A^GAAATCCCTGCGTCTGCGTGGAAGCGAGACGTGCACAGCA 183
Db     46  GGGTGCTGCGAGCTTTACCGAC.G:GAATCCGTCGCGTGGGACCCGGCCGTGTACAGCA 105

Qy    184  GACGAGCAGTGCCAGCAGTG^GCTCCGAGTAGTACGTGGCGGCCAATGGCCTGGGCC---- 239
Db    106  GACGAGCGCGTGCCAGCAGTGCGCTCTCTGAGTAGTACGTGGCACGATGCCTGGGGACGCG 165

Qy    240  -----GGGCTGGCGGGGACCCGGGAGCGTGGTGCGTGCCTCGCGGCCCGTGCCCTGCGC 294
Db    166  CCCCGGGCGGCAGGCGGGACCCGGGCGTGGGCTCCCGCGTGGCTGCTCCCGGATGGCGGC 225

Qy    295  CGCGTTCTTCGCGCGTGGGCGTCCGGCGGCTCACGCGAGGCTCTCTTCTGGCGGATGCGAA 354
Db    226  CGCGTTCTTCGCGCGTGGGCGTCCGGCGGCTCACGCGAGGCTCTCTTCTGGCGGATGCGAA 285

Qy    355  GGGCCCGCGTGCGCCGAGCGCCGGCGCCAGACAATTCGCGCGGGTTCCGGC 414
Db    286  GGCTTCGCGCGTGCGCCGAGCGCCAGACAGTTTCGCGCGGGTTCTCCGGC 345

Qy    415  CCCCAGCTGCGCCACCTTCCTGCTGAACGCCCTTGGACCGGTCGGAGCGAAAGCGCGGCCGG 474
Db    346  CCGGCGGTTGGTGCCCGCTCTTGCCTGGAGCCCGTTGGAGCGGCGCAGCGCGCCCTG 405

Qy    475  TGCCGCGGCCCGTCTCTT~GGCTTCCGAGGCCTCAGGCCCTCAGTGGCCTCTCCCGGAC 534
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Qy    535  GGCTGTCCGGAGGAGG:3GGCCCCGGGGTGTCTGCGCGCTCAGGCGCCTTGTAGGCACC 594
Db    466  CGCTGTCCCGGAGGAGGAGCCGGCCCCGGTTCGTCTCTGCGCGGCCTTGTAGGCACC 525

Qy    595  GTGGTCACCCCACTACCTGGACAACGTGAGCGGCGGGGGGCGGCCCCTGGTGCGCGCTGT 654
Db    526  GTGGTCACCCCAACTACCTGGACAACGTGAGCGGGCGCGGTTGGCCCTGGGTCGGCGTGT 585

Qy    655  GAGGCCCAGCGGGAAAGCGGGCGGGAGAGTGGGAAGGCTTCCGCCCAAGCTCTTTTACAAGGAAC 714
Db    586  GCGGCCCAGTGGGAAACCGGGGCGGAAATGGGAAGGCTTCCGCCAAGCTCTTTTACAAGGAAC 645

Qy    715  CCCTGCTTGGATGGT.GCCATACAACAAGCCTTGCACGTCTGCAACCATCAGTTCTGCAGGAC 774
Db    646  CCCTTGCTTGGATGGTTGCCATACAACAAGCCTTGCACCTTGCAACGCCATCAGTTCTGCAGGAC 705

Qy    775  CAGTGGAACCCCTACCAGAATGCTGGGGCCAGGGTTGGAGTGGGCCTGAGAA 834
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Qy    835  GAGATGCGGAGGCAGAAAACGGTCCCCGGTTTTGT------ 887
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Qy    948  CAGCTGA  954
Db    876  CAGCTGA  882
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RESULT 7

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LOCUS       MMU276514               810 bp    mRNA    linear    ROD 02-FEB-2001
DEFINITION  Mus musculus mRNA for putative GDNF family receptor alpha 4,
            GPI-anchored isoform (Gfra4 gene).
ACCESSION   AJ276514
VERSION     AJ276514.1  GI:7688056
KEYWORDS    GDNF family receptor alpha 4; Gfra4 gene; GPI-anchored isoform.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Lindahl,M., Timmusk,T., Rossi,J., Saarma,M. and Airaksinen,M.S.
  TITLE     Expression and alternative splicing of mouse Gfra4 suggest roles in
            endocrine cell development
  JOURNAL   Mol. Cell. Neurosci. 15 (6), 522-533 (2000)
  MEDLINE   20319126
   PUBMED   10860579
REFERENCE   2  (bases 1 to 810)
  AUTHORS   Airaksinen,M.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-MAR-2000) Airaksinen M.S., Program in Molecular
            Neurobiology, Institute of Biotechnology, P.O. Box 56 (Viikinkaari
            9), 00014 University of Helsinki, FINLAND
FEATURES             Location/Qualifiers
     source          1..810
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ORIGIN
      Query Match       58.9%;    Score 593.8;  DB 10;  Length 810;
      Best Local Similarity   90.2%;    Pred. No. 8.7e-91;
      Matches 650;  Conservative    0;  Mismatches  62;  Indels  9;  Gaps  1;

Qy     66  ACGGGTGCTGAAATGAGAGGGCCAGGGCCAGGGCAGTTTTATGGAGGTCTTGGATCGGACGAGGAGG 125
Db     15  ACATTTGATGGATGAGAGAGGGCCAGGGTCAGGGCTGAGTGGGGCCA 74

Qy    126  GTCAGCGGAGCTCCACTGAGGGAGAATCGCTCCGTGGAAGCAGCCGAGGCTGCACAGCAGA 185
Db     75  GTCTCGGAGCTTTACCGACGGGGAAATCGCTCCGTGGACGCGGCCGTGTACAGCAGCAGA 134
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RESULT 8
LOCUS       AX090389     834 bp    DNA    linear   PAT   21-MAR-2001
DEFINITION  Sequence 2 from Patent WO0116169.
ACCESSION   AX090389
VERSION     AX090389.1  GI:13444248
KEYWORDS
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Worley,D.
  TITLE     Ret ligand 5 (retl5) from human and mouse
  JOURNAL   Patent: WO 0116169-A 2 08-MAR-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
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misc_feature    656..716
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misc_feature    717..834
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Query Match       58.7%;  Score 591.8;  DB 6;  Length 834;
Best Local Similarity   87.2%;
Matches  711;  Conservative   0;  Mismatches   62;  Indels   42;  Gaps   4;

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Db   135  CGAGGCGGTGCCAGCAGCTGCCTCTGAGTACGTGGCACGATGGCCGCGGGCCAGCGCC         194

Qy   240  ---GGGCTGGCGGGGAGCTGGTGGTGGTCGCGCTCCCGCTGCCTCTGCCCTGCCTGG           296
             ||| |||| |||   ||||   |||| |||||||||||| ||||| ||||| ||||
Db   195  CGGGGCGGCAGGCGGACCGGGGCGGCCTCCCGCTCCCGCTCCCGCTGGGATGGGAAGG       254

Qy   297  CTTCTTCGCCGCCCGCGGCCTCAGCGACCACGCGGTCCTCTTCTTCTTCTGCGGCGGAAGG      356
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Db   255  CTTCTTCGCCGCCGTGGCCTCAGCGACACGCTCCTCTTCTGCGGCGGAAGG             314

Qy   357  CCCGGCGTGCCCGAGCGCGCCGCAGACATTCGGCGCGCCGTTCTCCGGCCCC              416
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Db   315  CTCCCGCCGTGGGCCCGAGCGCGGCCAGACTTTGGGCGCGCCGTTCTCCGGGCCC          374

Qy   417  CCAGGCTGGCGCGCCACCTTCCTCCTGAAGCCCTTGGACCGGCTGCGACGGAAGCCGCGGGTG    476
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Db   375  GGGGTTGGTGCGCGCCCTTGTGCCTGGAGGCGGCTGCGACGCAGCCGCGGCCTGTG        434

Qy   477  CCCGGCGGGCCGGCGTCTTTGCCTTCCAGCCTCATGCCTCCCGCGGCGGCGGGGACGG        536
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Qy   537  CTGGTCCGGAGGAGGGGGCCTACGGCAGGCGGGTGTCTGGCGCGGGTGGTGTGTAGGCACCGT   596
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Db   495  CTGCCCGGAGGAGGGGGCCGTGCTCAGCGTGCGGCTGCGGCACGGTCGCAGGCTCATAGGCACCGT 554

Qy   597  GGTCACCCGACCTACCTGAGCAACGTGAGCGGCCCGCGCGTGGTCGTCGGCTGTGTGA        656
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Db   555  GGTCACCCCAACTACCTGGACAACGTGAGCGGCCGCGTGGCGCCGTGGTGCGGCTGTGC       614

Qy   657  GGCCAGGCGGAAACGCGGCGGCGAAGAGTGCGGAAGCCGCCTGGGGCTTCTTCTGCGGATGGGAA 716
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Db   615  GGCCAGTGGAAACGCGGCAATGGAAGCCTTCCGCAGTGCTCACGCGCTCAGGCTCTTTTGACAGGAAACCC 674

Qy   717  CTGCTTGGATGTGCCATACAACAAGCCTTTGACAGCTTGCGCCCGTTCTGCAGGACCA         776
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Qy   777  G  777
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Db   735  G  735
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Qy   184  GACGAGCAGTGCCAGCAGCTGCGCTCCGAGTACGTGGCGCGCAATGCCTGGGGGC----       239
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Db   106  GACGAGCGGGTGCCAGCAGCTGCGGCTTCGAGTAGTACGTGGCGCACGGTGGGGCCAGCG      165

Qy   240  -----GGGCTGCGCGGGAGCTGCGTGGTGCCGCCGCGGCCCGGGGGCCGGCGCGC         294
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Db   166  CCCGGGGGACCCGGGGAGCTGCGCGGCGTGCGGCCCGCGTCCCGTGCGGCCCTGGC       225

Qy   295  CGCTTCTTCGCCCGGGGCCTCAGCGACCACGGCGGCTGCTTCTTCTTCTGCGGGGATGGGAA    354
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Qy   355  GGCCCCGCGGGGGGGGCCGGGGGCCGCGGGGCGCGCCGCCTCGGGGCCGGTTCTCCGGC       414
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Db   286  GGCTCCGCGGGGCGCGCGGGAGCTGCGCGGGACGTTTGGGCGCGCCGTTCTCCGGC       345

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Db   346  CCGGGGGTTGGGTCGGCGCCCTCTTGTGCCTGGAGCCCCTGCGGACGGCGCAGCCGCCGCTG    405

Qy   475  TGCCGGCGCCCCGTTCTTCTTTGCCTTCCAGGCCTCATCGCGCGGCTCCGCCGCGGCGGCAGC   534
          ||||| || ||||||||||| |||||||||| || |||  | |||| || |||||  ||| |
Db   406  TGCCGGCGCCCGTTCTTCCTTGCCTTCCAGGCCTCCCGCCGCGGCGCCGCCGCCGCCGGCGGAC 465

Qy   535  GGCTGTCCGGAGGAGGGGGGGGGCCCGGGCCGGTGTCTGCGGCGGCCGGGCCACC          594
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Db   466  CGCTGCCCGGAGGAGGGGGCCGCCGGGCGTTGTCTGCTACGGCCAGGGCGTCACGA        525

Qy   595  GTGGTCACCCCCAAACTACCTGGACAACGTGAGCGGCGTTGCGCCGTGGTGCGGCTGT       654
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Db   526  GTGGTCACCCCAACTACCTGGACAACGTGAGCGGCGTGGCGCCGTGGTGCGGCTGTGT       585

Qy   655  GAGGCCAGGCGGAAACCGGCGAAGAGTGCGGAAGCCGCCTTTCCGCAGCAGCTTTTACAAGGAAC 714
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Db   586  GCGGGCCAGTGGAAACCGGCGAAGAATGCGAAGCCTTCCGCAGCGCTCACGCGCTCAGGCT    645

Qy   715  CCCTGCTTGGATGTGCCATACAACAAGCCTTTGACAGCTTGCAACCATCAGTTCTGCAGGAC    774
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Db   646  CCCTGCTTGGATGGTGCCATACAACAAGCCTTTGACAGCTTGCAACCATCAGTTCTGCAGG--  703

Qy   775  CAGTGGAACCCCTACCAGATGCCTGGGCCAGGCGCCAGGTGGAGGCCTGAGTGGCCTGAGAA   834
          ||||||| ||||| |||  |||||||| ||||| ||||  ||||| || || || || |||
Db   704  C-------------ACCAGACTGCCTGGGCA----------------AGGCACGAGTGGCCTGAGAA    739

Qy   835  GAGATGGAGGCGAGAAAACGGTCCCCGGTTTTTGT--------------CCCAAGGTGTCCTGGATGTCCA    887
          ||||||||||| ||| || ||||||||||||| |              |||||| ||||| |||| | |
Db   740  GAGCTGGAGGCAGAAAACAGTCCTTGTTTTTGGTCCTACGCCCCAAGGTGTCCTGGCTGTATG        799
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RESULT 9

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LOCUS       AX090395                 783 bp    DNA        linear   PAT 21-MAR-2001
DEFINITION  Sequence 8 from Patent WO0116169.
ACCESSION   AX090395
VERSION     AX090395.1  GI:13444253
KEYWORDS
SOURCE      Mus sp.
ORGANISM    Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Worley,D.
TITLE       Ret ligand 5 (ret15) from human and mouse
JOURNAL     Patent: WO 0116169-A 8 08-MAR-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10095"
ORIGIN
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Query Match 55.4%; Score 558.2; DB 6; Length 783;
Best Local Similarity 91.4%;
Matches 606; Conservative 0; Mismatches 48; Indels 9; Gaps 1;

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Qy  124 GGGTCAGCGAGCTCCACTCACGGGGAAATCCCTGCCTGGGAAGCAGCCGAGGGTGTCACAGCA 183
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Db   46 GGGTTCTGCGAGCTTTACCGACGGGGAATCGGTGCGTGGACCGGCGGCCGAGGCGTGTACAGCA 105

Qy  184 GACGAGCAGTGCCAGCAGCTGCGCTCCGAGTAGCGGGGC---- 239
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Qy  240 ------GGGTCGGCGGGGACCCGGGACTGGGTGCGCGTGCGC 294
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Db  166 CCCGGAGCGCGAGGCCAGCCGGGACCCGGGGTGTGC 225

Qy  295 CGCTTCTTCCGGCCCCGCGGCCCCTCGCCGCTGCTCTTCTGCGGANTGCGAA 354
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Qy  355 GGGCCCGGCCGCTGGCGGGGGAGCTGGGTGGCGGCCAGC 414
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Db  286 GGCTTCGGCGTGCGGCCGAGCGCCCGAGACTTTCGCGCC 345

Qy  415 CCCCAGCTGGCGGCCACCTTCCTGCTGAAGCCCTTGGAC 474
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Db  346 CCCGGGGTTGGTGCGGCCGTGTCTGCGCGCGTTCCTGGA 405

Qy  475 TGCCGGGCCCCCGTCTCTCTTTGCCTTCCAGGCCGTA 534
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Qy  535 GGCTGTCCGGAGCGGAGGAGGGGGGGGGGGCGGCCACC 594
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Qy  595 GTGGTCACCCCAACTACCTGGACAAACGTGAGCGCGGGC 654
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Qy  655 GAGGCCAGCAGGGAAACCGGGGCGGCGAAGAGTCGGAAG 714
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Qy  715 CCCTGCTTGGATGGTGCCATACAAGCCTTTGACAGCTCGGCAACCATCAGTTCTGCAGGAC 774
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Db  646 CCCTGCTTGGATGGTGCCATACAAGCCTTTGACAGCCATCAGTTCTGCAGGAC 705
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RESULT 10

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LOCUS       MMU276870                783 bp    mRNA       linear   ROD 02-FEB-2001
DEFINITION  Mus musculus mRNA for GDNF family receptor alpha 4
            isoform (Gfra4 gene).
ACCESSION   MMU276870
VERSION     AJ276870.1  GI:7688066
KEYWORDS    alternative splicing; GDNF family receptor alpha 4; Gfra4 gene.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Lindahl,M., Timmusk,T., Rossi,J., Saarma,M. and Airaksinen,M.S.
TITLE       Expression and alternative splicing of mouse Gfra4 suggest roles in
            endocrine cell development
JOURNAL     Mol. Cell. Neurosci. 15 (6), 522-533 (2000)
MEDLINE     20319126
PUBMED      10860579
REFERENCE   2  (bases 1 to 783)
AUTHORS     Airaksinen,M.S.
TITLE       Direct Submission
JOURNAL     Submitted (20-MAR-2000) Airaksinen M.S., Program in Molecular
            Neurobiology, Institute of Biotechnology, P.O. Box 56 (Viikinkaari
            9), 00014 University of Helsinki, FINLAND
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
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     gene            1..783
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     CDS             1..783
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                     /function="putative binding receptor for persephin"
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Query Match 55.4%; Score 558.2; DB 10; Length 783;
Best Local Similarity 91.4%;
Matches 606; Conservative 0; Mismatches 48; Indels 9; Gaps 1;

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Db  646 CCCTGCTTGGATGGTGCCATACAAGCCTTTGACAGCCATCAGTTCTGCAGGAC 705
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Qy  775 CAG 777
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Db  706 CAG 708

Qy  124 GGGTCAGCGAGCTCCACTCACGGGGAAATCCCTGCCTGGGAAGCAGCCGAGGGTGTCACAGCA 183
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Db   46 GGGTTCTGCGAGCTTTACCGACGGGGAATCGGTGCGTGGACCGGCGGCCGAGGCGTGTACAGCA 105

Qy  184 GACGAGCAGTGCCAGCAGCTGCGCTCCGAGTAGCGGGGC---- 239
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Db  106 GACGAGCGCGTGCCAGCAGCTGCGCTTCTGAGTACGTGGGCCCGCAGCG 165
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RESULT 11

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LOCUS       AX090391                795 bp    DNA      linear   PAT 21-MAR-2001
DEFINITION  Sequence 4 from Patent WO0116169.
ACCESSION   AX090391
VERSION     AX090391.1  GI:13444250
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Worley,D.
  TITLE     Ret ligand 5 (retl5) from human and mouse
  JOURNAL   Patent: WO 0116169-A 4 08-MAR-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
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                     RVTAGLIGTVVTPNYLDNVSARVAPWCGCAAASGNRREECEAFRKLFTRNPCLDGAIQA
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ORIGIN

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Db    166 CCCGGGGGGCAGGGACCGGAGACTGCGTGCGGCGTTCCCGCTGCGGC 225

Qy    295 CGCTTCTTCCGCGCGCGCCCGGGGGGGCCGGGAGCTGCGTGCCGCTCACCGCCTCGCCGCTCCGCGGATCCGGA 354
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Db    226 CGCTTCTTCCGCGCGCGGGGCTTCCGGCGCGTCGCGATGCGGGCGGCTCACCGCTGCTTCTTCTGCGGGCTGGAA 285

Qy    355 GGCCCGGCGGTCGCGCCCAGCCCCGGGCCGGCCAGCATTGCGCCGCCTGCGCGCCCGCTTCTCCGGC 414
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Db    286 GGCTCCGGCGGTCGCGCCGAGCCCCGGAGACTTCGGCCGGCCCCAGACTTTCGGCGGTTCTCGGC 345

Qy    415 CCCCAGCTGCGCGCCGCCCACCTTCCTGCTTGCCCTGGGACCCCTTGGAGCGAAGCGCCGCGG 474
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Db    346 CCGGGGGTTGGTGCGCGCTCTTGCCTGCGCGCCCTTCTGGAGCGGCTGCCAGCCGCCGCCTG 405

Qy    475 TGCCGCGGCCCCGGTCTCCCTGCTTTGCCTTCAGGCCTTCATGGCTATGCCCTCCCCGCCCTCCCCGCCGAC 534
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    406 TGCCGCGGCCCCGGTCTCCCTGCTTTTGCCTTCAGGCCTTCATGGCTATGCCCTCCCCGCCCTCCCCGCCGAC 465

Qy    535 GGCTGTCCGGAGGAGGGGGGGGGGCCGGCCTACGCAGCAGGCGTGTAGGCACC 594
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    466 CGCTGCCCCGGAGGAGGGGGGGCCGGTTGTCTGCGCGGCCTCATAGGCCACC 525

Qy    595 GTGGTCACCCCCAACTACCTGGACAACGTGAGCGCGCGCGTCTCGACAACGTGCGGCGCTGT 654
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Db    526 GTGGTCACCCCCAACTACCTGGACAACGTGAGCGCGCGGTTGCGCCCCTGGTGTCGCGCTGT 585

Qy    655 GAGGGCCAGGCAGGGGAAAACGGGCGCGGAAGAGTGCAAGCCTTCCGCAAGCCTTCAAGGAAC 714
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Db    586 GCGGGCCAGTGGAAAACCGGGCGCGGAAGAATGCGAAGCCTTCCGCAAGCTCTTTACAAGGAAC 645

Qy    715 CCCTGCTTGATGGTGCCCATACAAGCCTTTGACAGTCGCAACCATCAGTTCTGCAGGAC 774
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Db    646 CCCTGCTTGGATGGTGCCATACAAGCCTTTGACAGTTCGCAACCATCAGTTCTGCAGGAC 705

Qy    775 CAG 777
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Db    706 CAG 708
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RESULT 12

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LOCUS       AX068323               2522 bp    DNA      linear   PAT 25-JAN-2001
DEFINITION  Sequence 5 from Patent WO0102557.
ACCESSION   AX068323
VERSION     AX068323.1  GI:12578506
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ORIGIN

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Best Local Similarity   88.5%;  Pred. No. 1e-76;
Matches  587;  Conservative    0;  Mismatches   49;  Indels   27;  Gaps    2;

Qy    124 GGGTCAGCGGAGCTCCACTGAGGGGGAAATCGGTCGGTGGAAAGCAGCGGCGGTGCACAGCA 183
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     46 GGGGTCTGCGAGCTTTACCGACGGGAAATCGGCTGGTGGACGCGGAGGCGGTGTACACGA 105

Qy    184 GACGAGCAGTGCCAGCAGCTGCCTCCGAGTACGTGGGCCAATGCCTGGGGCGGGCC----- 239
          ||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    106 GACGAGCGGTGCCAGCAGCTCTCGGAGTACGTGGCCAGCTGCCTCGGGCGCGCCGC 165

Qy    240 -----GGGCTGGCGGGGGGGGACCCGGGGAGCTGCGGTTGCGCGCCGCCTGCCCTGGC 294
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Db    166 CCCGGGGGGCAGGGGACCCGGGGGGGTGCGGCGTTCCCGCTGCGGC 225

Qy    295 CGCTTCTTCCGCGCGCGCCCGGGGGGGCCCGGGAGCTGCGGTGCCGCTCACCGCCTCGCCGGATGGAA 354
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Qy    355 GGCCCCGCGGTCGGGGCCGGCCGAGCCCCGGGCCGAGCAGACATTCGGCGCGCCCGGTTCTCCGGC 414
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Qy    415 CCCCAGCTGCGGCGCCGCCCACCTTCCTGCCTGGGAAGCCCTTTGGACCGGTCGGACGGAAGCCGCGT 474
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Db    346 CCGGGGGGTTGGTCGGCGCCACTTCTTGCCTGGCGGACGCGTTGCGAGCGGCAGCCGCTG 405

Qy    475 TGCCGCGCCCCCGGTCTCTTTGCCTTCCAGGCCTCATGGGCTCCCCCGGGGCCGGCCCCGGAC 534
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Db    406 TGCCGGTGC---------------GCCTCATGCGCTCCCCCGGCCGGCCCCGGCCCCGCCCGAC 447

Qy    535 GGCTGTCCGGAGGGAGGGGGCCCGCGCGGTGCTGCGCGCCTACGCCAGGCCTTGTAGGCACC 594
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Db    448 CGCTGCCCGGGGAGGGGGCCCCGGTTGTCTGCGCGGCCTCGCCAGGCCCTCATAGGCAC 507

Qy    595 GTGGTCACCCCCAACTACCTGGACAACGTGAGCGCGCGCGTTGCGCGGTTGCGCGCTGT 654
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Qy    655 GAGGGCCAGGCGGGAAAACGGGCGCGGAAGAGTGCGAAGCCTTCCGCAAGCTTTTACAAGGAAC 714
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Db    568 GCGGCCAGTGGAAAACCGGCGCGCAAGAAATGCGAAGCCTTCGCAAGCTTTTACAAGGAAC 627

Qy    715 CCCTGCTTGGATGGTGCCATACAAAGCCTTTGACAGTCGCAACCATCAGTTCTGCAGGAC 774
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Qy    775 CAG 777
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Db    688 CAG 690
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KEYWORDS   .
SOURCE     Rattus rattus (black rat)
  ORGANISM Rattus rattus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
           Rattus.
REFERENCE  1
  AUTHORS  Masure,S.L., Cik,M. and Hoefnagel,E.W.
  TITLE    Neurotrophic factor receptor gfr-alpha-4
  JOURNAL  Patent: WO 0102557-A 5 11-JAN-2001;
           JANSSEN PHARMACEUTICA N.V. (BE)
FEATURES             Location/Qualifiers
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ORIGIN

Query Match    45.1%;  Score 454.4;  DB 6;  Length 2522;
Best Local Similarity  82.3%;  Pred. No. 2.7e-67;
Matches  604;  Conservative  0;  Mismatches  1;  Indels  129;  Gaps  2;

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Db    683 AGGGTCAGCGAGCTTCCACTCAGGGGGAATCCTCGCTGGAGGCAGCGAGCGGTGCACAGC 742

Qy    183 AGAGGAGCAGTGCCAGCAGCAGCTGGGCGCTCCGAGTACGTGGCGGCTCCGGGCCGGGGG 242
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Db    743 AGAGGAGCAGTGCCAGCAGCAGCTGGGCCAATGGCCTGGGCCCGGGGCCGGGGCCGGGGG 802

Qy    243 CTGGCGGGGGAACCCGGAGGAGCTGGTGGTCGGCGGCGGGGCCCGGGGCGGGCCCTTCTT 302
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Db    803 CTGGCGGGGGAACCCGGAGGAGCTGGTGCTCGGCGGCGGGGCGGCGGGGGGGGCCCTTCTT 862

Qy    303 CGCCCGCGGCGGCCTCGGCGGCTCAGCACCACCGGCGTCTCTTCTTGCCGGATGCCGGGCC 362
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Db    863 CGCCCGCGGCGGCCTCGGCGGCTCACGCACCACCGGCGTCTCTTGCGGATGCCGGCAAGCC 922

Qy    363 GTCCGCGGCCCAGCGCGGCGGGGCCCAGACATTCGCGCCGCGTTCTCGCGGCCCCCCAGCT 422
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Db    923 GTGCCGCGGCCCAGCGCGGCGGGGCCCAGACATTCGCGGCGTTCTCCGGCCCCCCAGCT 982

Qy    423 GGGCCCACCTTCCTGCCTGAAGCCCTTGGACCGTGTGCGAGCGGAAGCCCGGGTGCC---- 478
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Db    983 GGGCCCACCTTCCTGCCTGAAGCCCTTGGACCGTGTGCGAGCGGAAGCCCGGGTGCCGGTG 1042

Qy    479 ----------------------------------------------------GGCCCGGTCTCTTTG 493
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Qy    494 CCTTCCAGCGCCTCAATGCGCTCCCGCGCGCGCGCGCGGCTCCCGGCGCCCGGGAGCAGCGG 553
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Qy    594 CGTTGGTCACCCCCCAACTACCTCGAGCAAACGTGAGCGGGTGCGCCTGCGGCCGGCTG 653
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Qy    714 CCCCTGCTTGGATG 727
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REFERENCE   1 (bases 1 to 245589)
  AUTHORS   Muzny,D.Marie., Metzker,M.lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
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            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
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            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
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            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE   Direct Submission
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 245589)
  AUTHORS   Worley,K.C.
  TITLE   Direct Submission
  JOURNAL   Submitted (15-SEP-2001) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3 (bases 1 to 245589)

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AUTHORS   Rat Genome Sequencing Consortium.
TITLE     Direct Submission
JOURNAL   Submitted (09-MAY-2003) Human Genome Sequencing Center, Department
          of Molecular and Human Genetics, Baylor College of Medicine, One
          Baylor Plaza, Houston, TX 77030, USA
COMMENT   On May 9, 2003 this sequence version replaced gi:2326476S.
          The sequence in this assembly is a combination of BAC based reads
          and whole genome shotgun sequencing reads assembled using Atlas
          (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
          in the feature table below represents a scaffold in the Atlas
          assembly (a 'contig-scaffold'). Within each contig-scaffold,
          individual sequence contigs are ordered and oriented, and separated
          by sized gaps filled with Ns to the estimated size. The sequence
          may extend beyond the ends of the clone and there may be individual
          contigs within a contig-scaffold that consist entirely of whole
          genome shotgun sequence reads. Both end sequences and whole genome
          shotgun sequence only contigs will be indicated in the feature
          table.
          --------- Genome Center
          Center: Baylor College of Medicine
          Center code: BCM
          Web site: http://www.hgsc.bcm.tmc.edu/
          Contact: hgsc-help@bcm.tmc.edu
          --------- Project Information
          Center project name: GBTI
          Center clone name: CH230-6D19
          --------- Summary Statistics
          Assembly program: Atlas;
          Consensus quality: 205514 bases at least Q40
          Consensus quality: 207203 bases at least Q30
          Consensus quality: 208050 bases at least Q20
          Estimated insert size: 221727; sum-of-contigs estimation
          Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
          -----
          * NOTE: Estimated insert size may differ from sequence length
          *  (see http://www.hgsc.bcm.tmc.edu/docs/genbank draft data.html).
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 1 contigs. Gaps between the contigs
          * are represented as runs of N. The order of the pieces
          * is believed to be correct as given, however the sizes
          * of the gaps between them are based on estimates that have
          * provided by the submittor.
          * This sequence will be replaced
          * by the finished sequence as soon as it is available and
          * the accession number will be preserved.
          * 1  245589: contig of 245589 bp in length.
FEATURES  Location/Qualifiers
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misc_feature   545..1006
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ORIGIN
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Best Local Similarity  82.3%;  Pred. No. 1.3e-67;
Matches  604;  Conservative  0;  Mismatches  1;  Indels  129;  Gaps  2;

Qy    123 AGGGTCAGCGAGCTCCACTGAGGGAATCGCTCGCGTGGAAGCAGCGCCCAGGCGCTGCACAGC  182
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Db  32217 AGGGTCAGCGAGCTCCACTGAGGGAATCGCTCGCGTGGAAGCAGCGCCCAGGCGCTGCACAGC  32276

Qy    183 AGACGAGCAGTGCCAGCGCTCCGAGTACGTGGCGCCAATGCCTGGGCGCCGGGCGGGG  242
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Db  32277 AGACGAGCAGTGCCAGCAGCTGCGCTCCGAGTACGTGGCGCCAATGCCTGGGCGCCGGGCGGGG  32336

Qy    243 CTGGGCGGGGACCCCGGAGAGCTGGGTGGGCCTCCGCGTTCCGCGTGCGCGCCGCCGCTCTT  302
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Db  32337 CTGGGCGGGGACCCCGGAGAGCTGGGTGGGCCTCCGCGTTCCGCGTGCGCGCCGCCGCTCTT  32396

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Qy    303 CGCCGCGGGCGGGGCCGTCCGGGCCTCACGACCACGACGCAGCGCTGCCCGGGGCCCCGC  362
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Qy    363 GTGCGCCGAGCGCCGCGGCCGCCAGACAATTCGCGCGGCCGGCCGGCCCCCCCCAGCT  422
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Db  32457 GTGCGCGCCGAGCGCCGCGGCCGCCAGACAATTCGCGCGGCCGGCCGGCCCCCCACGCT  32516

Qy    423 GCGCGCCACCTTCCTGCCTGAAGCCCTTGGACCGCTGCCGAGCCCGCCGCCCGGCGTG  478
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Db  32517 GCGCGCCACCTTCCTGCCTGAAGCCCTTGGACCGCTGCCGAGCCCGCCGCCCGGCGTG  32576

Qy    479 --------------------------------------------------GGCCCGTGCTCTTTG  493
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Db  32577 CGTGCGGGGGGGGGGCGGCTGGGCCTCACCGGGGTCCGGGGGCCCCGGTCGTCTTTG  32636

Qy    494 CCTTCCAGGGCTTCCGCTCCCGGGGCTCCCGGGGCCCGGGCGGACGCGCTGTCCGGAGAGG  553
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Db  32637 CCTTCCAGGGCTTCCATGGGGCTCCCGGGGCCCGGGCGGACGCGCTGTCCGGAGAGGGGG  32696

Qy    554 GCCCGCGGGGTGTCTGCGGGCCCTACGCCAGGCCTTGT-----------  587
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Db  32697 GCCCGCGGTGTCTGCGGGCCCTACGCCAGGCCTTGTAGGTACGCGCTGGGGGCCGGG  32756

Qy    588 ------------------------------------------AGGCAC  593
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Db  32757 CGGGGCGGGGAGGCAGAGGCAGGATTCCGGGGGGCCCGTCACAGGTCCTGGGGGTCCCAGGCAC  32816

Qy    594 CGTGGTCACCCCCAACTACCTGGACAACGACGCCGCCGCCGTTGCGCCCCTGGTGCGCGCTG  653
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Db  32817 CGTGGTCACCCCCAACTACCTGGACAACGACGTGAGCGCGGTTGCGCCCCTGGTGCGCGGCTG  32876

Qy    654 TGAGGGCCAGCGCGAAAACCGGGCGCCGGAGAGGTGGCGAAGAGCCTTCCGCAAGCTTTTTACAAGGAA  713
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Db  32877 TGAGGGCCAGCGGAAAACCGGGCGCCGGAAGAGTGCGAAGAGCCTTCCGCAAGCTTTTTTACAAGGA  32936

Qy    714 CCCCTGCTTTGGATG  727
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Db  32937 CCCCTGCTTTGGGGTG  32950
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RESULT 14
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LOCUS       AF253318        1427 bp    mRNA      linear   PRI 25-OCT-2000
DEFINITION  Homo sapiens GFR receptor alpha 4 protein (GFRA4) mRNA, complete
            cds.
ACCESSION   AF253318
VERSION     AF253318.1   GI:10998399
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1427)
AUTHORS     Zhou,B., Levinson,B. and Gitschier,J.
TITLE       Direct Submission
JOURNAL     Submitted (06-APR-2000). Department of Medicine, University of
            California, 533 Parnassus Ave, San Francisco, CA 94143, USA
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ORIGIN
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Query Match        42.7%;  Score 430.6;  DB 9;  Length 1427;
Best Local Similarity 73.2%;  Pred. No. 3.2e-63;
Matches 595;  Conservative 0;  Mismatches 184;  Indels 34;  Gaps 2;

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Qy  184 GACGAGCAGTGCCACAGCTGCGCGTCCGAGGTACGTGGCGCGCAATGCCTGGGCGCGGGGC  243
            |||| || || ||| | ||| ||||||||| | ||||| ||| | |||||||||||||||
Db  106 GACCGCGCGGTGCCACGGTTTGCGCTCCGAGTATGTGGCCGGAGTGCCTGGGCGGGGGC--- 161

Qy  244 TGGCCGGGGACCCGGGGAGCTGCGTGGCCGCTGCCCGTGCCCGTGCCCTGGGCGGTTCTTC 303
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Db  162 -----TGCCCAGGGGGGCGGCGTGTCCCCAGGTCGTCCCCTCCCGCGCGGCCGCGTTCTTC 216

Qy  304 GCCGCGGGCGCTCCGGCGCTCACGCACGCGCCCGCCCCCGCCGTGCCCCTGGGCGGTTCTTC 363
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Qy  364 TGGCCCGGAGCGCGCGGCGCAGACATTCGCGGGCGCGGTTCTCCGCCAGCTG 423
Db  277 TGCCCGGAGCGTCGGGCGCCAGACCTTCGTGTCCTGCGCCTTTTCGGGGCCC 336

Qy  424 GCGCGCACCTTCCTCGGCTGAAGCCTGTGGAGCGCGCGGTGCCGGGCGCCCC 483
Db  337 GCCCCGGGCCTCCCGGCGCCCTTAAACTTCTGCGAGCGCGTCTGCAGGGCCT 396

Qy  484 CGTCTCTTTGCCTTCCAGGGCCTCATGGGCTCCCGCGACGGCTGTCCG 543
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Qy  544 GAGGAGGGGGGGCGCGGGGTGTCTCGCGGGCCGCTAGGCCACGGTGGTCACC 603
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LOCUS       HSA291673               810 bp    mRNA    linear   PRI 20-MAR-2001
DEFINITION  Homo sapiens mRNA for GDNF family receptor alpha 4, GPI anchored
            isoform (GFRA4 gene).
ACCESSION   AJ291673
VERSION     AJ291673.1  GI:12038956
KEYWORDS    GDNF family receptor alpha 4, GPI anchored isoform; Gfra4 gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lindahl,M., Poteryaev,D., Yu,L., Arumae,U., Timmusk,T.,
            Bongarzone,I., Aiello,A., Pierotti,M.A., Airaksinen,M.S. and
            Saarma,M.
  TITLE     Human glial cell line-derived neurotrophic factor receptor alpha 4
            is the receptor for persephin and is predominantly expressed in
            normal and malignant thyroid medullary cells
  JOURNAL   J. Biol. Chem. 276 (12), 9344-9351 (2001)
  MEDLINE   21153758
   PUBMED   11116144
  REMARK    online publication 10.1074/jbc.M008279200
REFERENCE   2  (bases 1 to 810)
  AUTHORS   Airaksinen,M.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2000) Airaksinen M.S., Program in Molecular
            Neurobiology, Institute of Biotechnology, P.O. Box 56 (Viikinkaari
            9), 00014 University of Helsinki, FINLAND
FEATURES             Location/Qualifiers
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                     /tissue_type="thyroid"
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ORIGIN
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Query Match        42.4%;  Score 427.6;  DB 9;  Length 810;
Best Local Similarity 77.2%;  Pred. No. 1.1e-62;
Matches 536;  Conservative 0;  Mismatches 149;  Indels 9;  Gaps 1;

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Db   46 GGGTCGGCGAGCTCGGTCGGAGGGAACCGATGTGTGGACACGGCCCGAAGCCTGCACGGCG  105

Qy  184 GACGAGCAGTGCCACAGCTGCGCGTCCGAGGTACGTGGCGCGCAATGCCTGGGCGCGGGGC  243
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Db  106 GACCGCGCGGTGCCACGGTTTGCGCTCCGAGTATGTGGCCGGAGTGCCTGGGCGGGGGC--- 161

Qy  244 TGGCCGGGGACCCGGGGAGCTGCGTGGCCGCTGCCCGTGCCCGTGCCCTGGGCGGTTCTTC 303
                 |||| ||||   | | |||||| ||  | ||| | | |||  ||||| ||||||
Db  162 -----TGCCCAGGGGGGCGGCGTGTCCCCAGGTCGTCCCCTCCCGCGCGGCCGCGTTCTTC 216
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Qy    304 GCCCCGCGGGGGCCTTCCCGGGGGGCTCACGGCAGCGGGCGTTGGCTCTTCTTCTGGGGATGGCGAAGGCCCCGCG 363
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Db    217 GCCCCGCGGGGGCCCCCCGGGGGGCTCACCCAGCGACTGCTCTTTCTGCCGTGGCGCGGGGGCCCCCGGCG       276

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Qy    424 GCGCCACCTTCCTGCTTGAACGCCCCTGGGACGCCGGGCGAAAGCGCCCGGTTGCCCGGCCC 483
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Qy    484 CGTCTCTTTGCCTTCCAGGGCTTCATGGGCCTCCCGGGCCCCCGGGCCTCCCCGCGACCGGCTGTCCG 543
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Db    397 CGCCTTCCTGGCCTTTCAGGTCTTCGGTGCACCCCCAGCGCCCCCCGACGGGCTGCCCTG       456

Qy    544 GAGGAGGGGGGCCCGCGTGTCTGCGCGCCCTAGCGACGCCTTGTAGGCACCGTGGTCACC 603
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Db    457 CTGGACCAGGGGCCCCCGCCTGCCTGCCTCGGGGGCACCCCCGTCACC                  516

Qy    604 CCCAACTACCTGGACAAACGTGAGCGGGGCGGGGCCGTTGCCCCTCGGTGCGCGGCTCGTTGAGGGCCAGC 663
          || ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    517 CCTAACTACGTGGACAAACGTGAGGCGCCGCGTGGGCGGCCCTGGTGCCGGACTCGCGGACCAGC        576

Qy    664 GGAAACCGGCGGCGAAGAGTGCGAAGCCTTCCCAAGCTTTTTTACAAGGAACCCCTGCTTG 723
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Db    577 GGGAACCGGCGGCGTGAGGAACTGCGGAAGCCTTCCGGGGGGGCTTCTTTACCAGGAACCGGCTGCTTG 636

Qy    724 GATGGTGCCATACAAGCCTTTGACAGCTTCGCAAACCATCAGTTCTGCAGGACCAGTGGAAC 783
          ||||||||||||||||||||| ||||| |||||| ||||||||||||||||||||
Db    637 GATGGTGCCATTCAGGGCCTTTGCCAGCGGGGTTGGCCCCCAGTCCCGCTGCTGGACCAGCTGAAC 696

Qy    784 CCCTACCAGGAATGCTCGGGCGCAGGCCCAAGGTGGAGG 817
          || |||||||||||||||||| ||||||||
Db    697 CCCCAGGGGAGACCCGGAGCACAGCCCTCCTGCCAGG 730
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OM nucleic - nucleic search, using sw model.

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                                GenCore version 5.1.6
                                Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:           February 18, 2005, 00:54:05 ; Search time 698 Seconds
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Title:            US-10-019-337E-7
Perfect score:    1008
Sequence:         1 ctggtaagcttaaggcaga.........aactcccttgccctcaggtc 1008
Scoring table:    IDENTITY NUC
                  Gapop 10.0, Gapext 1.0
Searched:         4390206 seqs, 295987.0667 residues

Total number of hits satisfying chosen parameters:       8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        N_Geneseq_16Dec04:*
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                  5: geneseqn2001bs:*
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                 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	872	86.5	953	4	AAF31062	Aaf31062 Rat GFRal
3	630.6	62.6	882	4	ABL51670	Abl51670 Mouse put
4	591.8	58.7	834	4	AAF57270	Aaf57270 Mouse Ret
5	558.2	55.4	783	4	AAF57273	Aaf57273 Mouse Ret
6	558.2	55.4	783	4	ABL51669	Abl51669 Mouse GPI
7	510.6	50.7	795	4	AAF57271	Aaf57271 Mouse Ret
8	487.2	48.3	1019	2	AAZ28259	Aaz28259 Murine gl
9	454.4	45.1	2522	4	AAF31061	Aaf31061 Rat GFRal
10	427.6	42.4	810	4	ABL51672	Abl51672 Human GPI
11	427.6	42.4	849	4	AAF57272	Aaf57272 Human Ret
12	356.8	35.4	15914	4	AAF57269	Aaf57269 Mouse Ret
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14	313.6	31.1	573	4	ABL51671	Abl51671 Mouse sec
15	299.6	29.7	995	4	AAD10139	Aad10139 Mouse Gdn
16	299.6	29.7	995	6	ABL35075	Abl35075 Murine CD
17	291.4	28.9	549	4	ABL51674	Abl51674 Human put
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19	258.8	25.7	792	4	AAF31057	Aaf31057 Murine ES
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 c 23 216.4 21.5 207433 12 ADL81193 Adl81193 BAC1098L2
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   26 209   20.7 872     4 AAF31058 Aaf31058 Murine ES
   27 202   20.0 497     4 AAZ91456 Aaz91456 Human neu
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   29 150.4 14.9 1392    6 ABK50453 Abk50453 Human neu
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   31 150.4 14.9 1392   10 AAX01741 Aax01741 Human GDN
   32 150.4 14.9 1490    2 AAV64342 Aav64342 Human TGF
   33 150.4 14.9 1543    2 AAV99332 Aav99332 Glial cel
   34 150.4 14.9 1543    2 AAA64145 Aaa64145 Nucleotid
   35 150.4 14.9 1646    3 AAF98442 Aaf98442 Human CDN
   36 150.4 14.9 1646    3 AAV00248 Aav00248 Human Ret
   37 150.4 14.9 1888    2 ADJ58704 Adj58704 Human ret
   38 150.4 14.9 1888   12 AAV58006 Aav58006 Human neu
   39 150.4 14.9 1995    6 ABN87360 Abn87360 Human NTN
   40 150.4 14.9 1995    3 AAZ91459 Aaz91459 Human NTN
   41 150.4 14.9 1995    6 ABL41778 Abl41778 DNA seque
   42 150.4 14.9 1995    6 ABK50456 Abk50456 Human NTN
   43 150.4 14.9 1995   10 ADD11666 Add11666 Human NTN
   44 150.4 14.9 2600    2 AAV58004 Aav58004 Human neu
   45 150.4 14.9 2600    2 AAV58004 Aav58004 Human neu
```

ALIGNMENTS

```
RESULT 1
AAF31063
ID   AAF31063 standard; cDNA; 1008 BP.
XX
AC   AAF31063;
XX
DT   06-APR-2001  (first entry).
XX
DE   Rat GFRalpha-4 splice variant B coding sequence.
XX
KW   Rat; GFRalpha-4; carcinoma; familial hirschsprung disease; pain;
KW   glial cell-line derived neurotrophic factor; neurodegenerative disease;
KW   GDNF family receptor alpha-4; Alzheimer's disease; Parkinson's disease;
KW   motor neuron disease; peripheral neuropathy; spinal cord injury;
KW   chromosome 3q36; ss.
OS   Rattus rattus.
XX
PN   WO20010102557-A1.
XX
PD   11-JAN-2001.
XX
PF   26-MAY-2000 ; 2000WO-EP004918.
XX
PR   29-JUN-1999;   99GB-0001500.
XX
PA   (JANC ) JANSSEN PHARM NV.
XX
PI   Masure SLJ,  Cik M,  Hoefnagel EW;
XX
DR   WPI; 2001-138137/14.
DR   N-PSDB; AAB61637.
XX
PT   Glial cell-line derived neurotrophic factor family receptor alpha-4,
PT   useful for preparing medicaments for treating neurodegenerative diseases
PT   (e.g. Alzheimer's disease, Parkinson's disease) and carcinomas.
XX
PS   Claim 6; Page 72-73; 82pp; English.
XX
CC   The present invention relates to rat Glial cell-line Derived Neurotrophic
CC   Factor (GDNF) family receptor alpha-4 (GFRalpha-4; see AAB61636 and
CC   AAB61637). The present sequence is the coding sequence for rat GFRalpha-4
CC   splice variant B. GFRalpha-4 is useful in the preparation of a medicament
```

```
CC  for the treatment of neurodegenerative diseases, Alzheimer's disease,
CC  Parkinson's disease, motor neuron disease, peripheral neuropathy, spinal
CC  cord injury, familial hirschsprung disease, carcinomas, and diseases
CC  associated with GFRalpha-4 receptor dysfunction and in alleviating pain.
CC  The rat GFRalpha-4 gene is localised on chromosome 3q36
XX
SQ  Sequence 1008 BP; 173 A; 327 C; 327 G; 181 T; 0 U; 0 Other;

Query Match             100.0%;  Score 1008;  DB 4;  Length 1008;
Best Local Similarity   100.0%;  Pred. No. 3.2e-205;
Matches 1008;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 CTGGTAAGCTTTAAGGCAGAGGAGGAGGAGAGCTAAGAGCTGAGACATGCTYATGTTGAGTGGAGCG  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CTGGTAAGCTTTAAGGCAGAGGAGGAGGAGAGCTAAGAGCTGAGACATGCTYATGTTGAGTGGAGCG  60

Qy    61 TATTTACGGGTGCTGAAATGAGAGGAGGAGGCCAGGCAGTTTTATGGAGTCTTGGATGCCAG    120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TATTTACGGGTGCTGAAATGAGAGGAGGAGGCCAGGCAGTTTTATGGAGTCTTGGATGCCAG    120

Qy   121 AGAGGGTCACCGAGTCCACTGAGGGGAATCGCTCGTGTGAAGCAGCCCGAGGGCGTTGCACA   180
Db   121 AGAGGGTCACCGAGTCCACTGAGGGGAATCGCTCGTGTGAAGCAGCCCGAGGGCGTTGCACA   180

Qy   181 GCAGACGAGCAGTGCCAGCAGCTGCCGCTCCGAGTACGTGGCGCAATGCTGGGCGCCGGGCG   240
Db   181 GCAGACGAGCAGTGCCAGCAGCTGCCGCTCCGAGTACGTGGCGCAATGCTGGGCGCCGGGCG   240

Qy   241 GGCTGCGCGGGGAGCCCGGGAGCTGCGTGCGCTGCGCCCGCGTGCCCGCCGCCGCGCCGCTTC  300
Db   241 GGCTGCGCGGGGAGCCCGGGAGCTGCGTGCGCTGCGCCCGCGTGCCCGCCGCCGCGCCGCTTC  300

Qy   301 TTCGCCCGCGGCGGCTTCGCGGGGCCTCAGCGACGCGCTGCTCTTCTGTCGGCGGAAGGCCCC   360
Db   301 TTCGCCCGCGGCGGCTTCGCGGGGCCTCAGCGACGCGCTGCTCTTCTGTCGGCGGAAGGCCCC   360

Qy   361 GCGTCGCCGAGCGCGCCGCCCAGACATTCGCACGCGCGGTTCTCCGGCCCCCAG           420
Db   361 GCGTCGCCGAGCGCGCCGCCCAGACATTCGCACGCGCGGTTCTCCGGCCCCCAG           420

Qy   421 CTGGCGCCCACCTTCCTGCCCTGGAACCGCGGAGCCGCCCGCGTGCCGG          480
Db   421 CTGGCGCCCACCTTCCTGCCCTGGAACCGCGGAGCCGCCCGCGTGCCGG          480

Qy   481 CCCCGTCTCTTTTGCCTTCCAAGGCCTCAGTGCGCCTCCGCGCCGCGGCTGT           540
Db   481 CCCCGTCTCTTTTGCCTTCCAAGGCCTCAGTGCGCCTCCGCGCCGCGGCTGT           540

Qy   541 CCGGAGGAGGGGGGCCGGTGTCGTGGGGCCTACCGACACCGTGGTC                600
Db   541 CCGGAGGAGGGGGGCCGGTGTCGTGGGGCCTACCGACACCGTGGTC                600

Qy   601 ACCCCCAACTACCTGGACAACGTGACGCGCGGCGGTTGGGCGGCC                 660
Db   601 ACCCCCAACTACCTGGACAACGTGACGCGCGGCGGTTGGGCGGCC                 660

Qy   661 AGCCGAAACCGGCGGAAGACTGCGAAGCCTTCCCGCAAGCTTTTTCAAGGAAACCCCTGC  720
Db   661 AGCCGAAACCGGCGGAAGACTGCGAAGCCTTCCCGCAAGCTTTTTCAAGGAAACCCCTGC  720

Qy   721 TTGGATGGTGCCATACAAAGCCTTTGACAGTCGCAACCATCAGTTCTGCAGGACCAGTGG  780
Db   721 TTGGATGGTGCCATACAAAGCCTTTGACAGTCGCAACCATCAGTTCTGCAGGACCAGTGG  780

Qy   781 AACCCCTTACCAGAATGCTGGGCGGCCAAGGTGGCGGCCTGAGATGGAGACAGAGATG    840
Db   781 AACCCCTTACCAGAATGCTGGGCGGCCAAGGTGGCGGCCTGAGATGGAGACAGAGATG    840

Qy   841 GAGGCAGAAAACGGTCCCGGTTTTGTCCAAGGTGTCCTCGATGTCCATACTCACTGCCCCT  900
Db   841 GAGGCAGAAAACGGTCCCGGTTTTGTCCAAGGTGTCCTCGATGTCCATACTCACTGCCCCT  900

Qy   901 GGCTCTCCAGGCCCTGCTCTAATTAGGAAGGTGACCATGGACACACACTGACTGCCA    960
```

```
Db   901 GGCTCTCCAGGCCCTGCTCTAATTAGGAAGGTGACCATGGACACACACTGACTGCCA    960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   961 TGTCTCTGGATTATGCTCACTGAACTGAAACTCCCTTGCCCCTCAGGTC  1008
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TGTCTCTGGATTATGCTCACTGAACTGAAACTCCCTTGCCCCTCAGGTC  1008
```

```
RESULT 2
AAF31062
ID   AAF31062 standard; cDNA; 953 BP.
AC   AAF31062;
XX
DT   06-APR-2001  (first entry)
XX
DE   Rat GFRalpha-4 splice variant A coding sequence.
XX
KW   Rat; GFRalpha-4; carcinoma; familial hirschsprung disease; pain;
KW   glial cell-line derived neurotrophic factor; neurodegenerative disease;
KW   GDNF family receptor alpha-4; Alzheimer's disease; Parkinson's disease;
KW   motor neuron disease; peripheral neuropathy; spinal cord injury;
KW   chromosome 3q36; ss.
XX
OS   Rattus rattus.
XX
PN   WO200102557-A1.
XX
PD   11-JAN-2001.
XX
PF   26-MAY-2000; 2000WO-EP004918.
XX
PR   29-JUN-1999; 99GB-00015200.
XX
PA   (JANC ) JANSSEN PHARM NV.
XX
PI   Masure SLJ, Cik M, Hoefnagel EW;
XX
DR   WPI; 2001-138137/14.
DR   P-PSDB; AAB61636.
XX
PT   Glial cell-line derived neurotrophic factor family receptor alpha-4,
PT   useful for preparing medicaments for treating neurodegenerative diseases
PT   (e.g. Alzheimer's disease, Parkinson's disease) and carcinomas.
XX
PS   Claim 6; Page 72; 82pp; English.
XX
CC   The present invention relates to rat Glial cell-line Derived Neurotrophic
CC   Factor (GDNF) family receptor alpha-4 (GFRalpha-4; see AAB61636 and
CC   AAB61637). The present sequence is the coding sequence for rat GFRalpha-4
CC   splice variant A. The present sequence is useful in the preparation of a medicament
CC   for the treatment of neurodegenerative diseases, Alzheimer's disease,
CC   Parkinson's disease, motor neuron disease, peripheral neuropathy, spinal
CC   cord injury, familial hirschsprung disease, carcinomas, and diseases
CC   associated with GFRalpha-4 receptor dysfunction and in alleviating pain.
CC   The rat GFRalpha-4 gene is localised on chromosome 3q36
XX
SQ   Sequence 953 BP; 156 A; 314 C; 306 G; 177 T; 0 U; 0 Other;

Query Match             86.5%;  Score 872;  DB 4;  Length 953;
Best Local Similarity   93.6%;  Pred. No. 3e-176;
Matches 943;  Conservative  0;  Mismatches  10;  Indels  55;  Gaps  1;

Qy     1 CTGGTAAGCTTTAAGGCAGAGGAGGAGGAGAGCTAAGAGCTGAGACATGCTYATGTTGAGTGGAGCG  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CTGGTAAGCTTTAAGGCAGAGGAGGAGGAGAGCTAAGAGCTGAGACATGCTYATGTTGAGTGGAGCG  60

Qy    61 TATTTACGGGTGCTGAAATGAGAGGAGGAGGCCAGGCAGTTTTATGGAGTCTTGGATGCCAG    120
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TATTTACGGGTGCTGAAATGAGAGGAGGAGGCCAGGCAGTTTTATGGAGTCTTGGATGCCAG    120

Qy   121 AGAGGGTCAGGCGAGCTCCACTGAGGGGAATCGCTCGTGCGTGGAAGACGCCGAGGGCGTGCACA  180
         |||||||||
Db    61 TATTTACGGGTGCTGAAATGAGAGGAGGAGGCCAGGCAGTTTTATGGAGTCTTGGATGCCAG    120
```

Db 121 AGAGGGTCACGAGCTCCACTGAGGGGAATCGCTCGCGTGGACGCGGCGACGAGGCGTGCACA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 181 GCAGACGAGCAGTGCCAGCAGCTGCGCTCCGAGTACGTGGCGCAATGCCTGGGCCGGGGCG 240

Db 181 GCAGACGAGCAGTGCCAGCAGCTGCGCTCCGAGTACGTGGCGCAATGCCTGGGCCGGGGCG 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 241 GGCGTGGCGGGGGACCCGGGAGCTGCGTCGCTCCCCGGGCGCCTGCGCGCGCCGCGCTTC 300

Db 241 GGCGTGGCGGGGGACCCGGGAGCTGCGTCGCTCCCCGGGCGCCTGCGCGCGCCGCGCTTC 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 301 TTCGCGCCGCGCGGGGGGCTTCACGCACGCACGCACGCACGCGGGATCGGAAGGCCCC 360

Db 301 TTCGCGCCGCGCGGGGGGCTTCACGCACGCACGCACGCACGCGGGATCGGAAGGCCCC 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 361 GCCGTGCGCGCCCAGCGGCGCGCGGAGCTCACGCACGCGCTCTTCTCGGGATCGGAA 420

Db 361 GCCGTGCGCGCCCAGCGGCGCGCGGAGCTCACGCACGCGCTCTTCTCGGGATCGGAA 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 421 CTGGCGCGCCACTTCCTGCCTGAAGGCCCTTGGACCCCTGTGCGAGAGCGAAGCGGCCG 480

Db 421 CTGGCGCGCCACTTCCTGCCTGAAGGCCCTTGGACCCCTGTGCGAGAGCGAAGCGGCCG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 481 CCCGGTCTCTTTTGCTTTCCAGGCCTTCATGCGGGCGCTGGTCCCCGGACGGCTGT 540

Db 481 CCCGGTCTCTTTTGCTTTCCAGGCCTTCATGCGGGCGCTGGTCCCCGGACGGCTGT 540
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy 541 CCGGAGGAGGGGGGCCCGGGTGTCTGCGGGCCTACGCACGCCCCGGGCGGGCGCGG 600

Db 541 CCGGAGGAGGGGGGCCCGGGTGTCTGCGGGCCTACGCACGCCCCGGGCGGGCGCGG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 601 ACCCCCAACTACCTGGACAACGTGAGGCGCGGCGGTTGCGGCGGCGCTGTGAGGCC 660

Db 601 ACCCCCAACTACCTGGACAACGTGAGGCGCGGCGGTTGCGGCGGCGCTGTGAGGCC 660
         |||||||||||||||||||||||||||||||||||||||||||||||
Qy 661 AGCGGAAACGGCGCGGAAGAGTGCGGAAGCCTTCCGCGAAGCTTTTTACAAGGAA 720

Db 661 AGCGGAAACGGCGCGGAAGAGTGCGGAAGCCTTCCGCGAAGCTTTTTACAAGGAA 720
         ||||||||||||||||||||||||||||||||||||||||||||||
Qy 721 TTGGATGGTGCCATACAAGCTTTGACAGCTTCGCAACCATCAGTTCTGCAGGAC 780

Db 721 TTGGATGGTGCCATACAAGCTTTGACAGCTTCGCAACCATCAGTTCTGCAGGAC 780
         |||||||||||||||||||||||||||||||||||||||||||||
Qy 781 AACCCCTACCAGAATGCTGGGCGAGGCCAAGGTGGACACGCTGACTACG 840

Db 781 AACCCCTACCAGAATGCTGGGCGAGGCCAAGGTGGACACGCTGACTACG 840
         |||||||||||||||||||||||||||||||||||||||||-----
Qy 841 GAGGCGAGAAACGGGTCCCCGGTTTGTCCCAAGGTGTCCTCCAAGTTCCA 900

Db 841 GAGGCGAGAAACGGGTCCCCGGTTTGTCCCAAGGTGTCCTCCAAGTTCCA 900
         |||||||||||||||||||||||||||||||||||||||||
Qy 901 GGCTTCTCCAGGCCCTGCTCTAATTAGGAGTGAACCATGGACACAACAGC 960

Db 846 GGCTTCTCCAGGCCCTGCTCTAATTAGGAGTGAACCATGGACACAACAGC 905

Qy 961 TGTCTCTGGATTATGCTCACTGAACTGAAACTCCCTTGCCCTCAGGTC 1008
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 906 TGTCTCTGGATTATGCTCACTGAACTGAAACTCCCTTGCCCTCAGGTC 953

KW medullary thyroid carcinoma; pheochromocytoma; parathyroid hyperplasia;
KW neuronal disorder; aberrant axonal sprouting; gene; ss.
XX
OS Mus musculus.
XX
FH Key   Location/Qualifiers
FT
FT CDS   1..882
FT   /*tag= a
FT   /product= "transmembrane isoform a2"
XX
PN WO200162795-A1.
XX
PD 30-AUG-2001.
XX
PF 14-NOV-2000; 2000WO-FI000994.
XX
PR 21-FEB-2000; 2000FI-00000394.
XX
PA (LICE-) LICENTIA LTD.
XX
PI Airakainen M, Saarma M, Poteriaev D, Lindahl M, Timmusk T;
PI Rossi J;
XX
PT New nucleic acid sequence for manufacturing polypeptides for treating
PT endocrine cancers comprises a cDNA encoding a splicing isoform of
PT mammalian growth factor receptor (GPR)alpha4.
XX
PS Claim 4; Fig 19A; 143pp; English.
XX
CC The present invention describes an isolated and purified cDNA sequence
CC encoding a splicing isoform of a mammalian growth factor receptor
CC (GPR)alpha4, or its fragments. GFRalpha4 sequences have cytostatic,
CC osteopathic, neuroprotective and anticonvulsant activities. GFRalpha4 is
CC a glycosyl-phosphatidylinositol (GPI)-linked glial cell line-derived
CC neurotrophic factor (GDNF) family alpha-receptor. A GFRalpha4
CC polynucleotide sequence can be used for recording GFRalpha4 mediated
CC signalling in neurons or endocrine cells such as thyroid calcitonin-
CC producing C-cells, parathyroid gland cells, adrenal chromaffin cells, or
CC cells from the pituitary intermediate lobe. GFRalpha4 protein and
CC polynucleotide sequences can be are used for manufacturing polypeptides
CC useful for diagnosing and/or treating tumours in parathyroid gland cells,
CC adrenal chromaffin cells, cells of pituitary intermediate lobe,
CC neoplasia, endocrine tumours, medullary thyroid carcinoma and
CC pheochromocytoma, parathyroid hyperplasia, neuronal disorders or for
CC preventing neuronal death or aberrant axonal sprouting. The present
CC sequence encodes the mouse GFRalpha 4 protein, designated transmembrane
CC isoform a2, from the present invention
XX
SQ Sequence 882 BP; 121 A; 303 C; 296 G; 162 T; 0 U; 0 Other;

Db RESULT 3
ID ABL51670
    ABL51670 standard; cDNA; 882 BP.
XX
AC ABL51670;
XX
DT 08-JUL-2002 (first entry)
XX
DE Mouse putative transmembrane isoform a2 encoding cDNA SEQ ID NO:8.
XX
KW GFRalpha4; glycosyl-phosphatidylinositol; GPI; GDNF; cytostatic;
KW glycosyl-phosphatidylinositol-linked GDNF family alpha-receptor;
KW glial cell line derived neurotrophic factor; osteopathic; tumour;
KW neuroprotective; anticonvulsant; neoplasia; endocrine tumour;

Query Match   62.6%; Score 630.6; DB 4; Length 882;
Best Local Similarity 87.0%; Pred. No. 7.9e-125;
Matches 737; Conservative 0; Mismatches 84; Indels 26; Gaps 3;

Qy 124 GGGTCACGAGCTCCACTGAGGGGAATCGCTCGCGTGGACGCGGCGACGAGGCGTGCACAGCA 183
         |||||| |||| |||||||||||||||||||||||||||||||||||||||||||||
Db 46   GGGTCTGCCGAGCTTTACCGACGGGAATCGCTCGCGTGGACCGCGCCGAGGCGGTACAGCA 105

Qy 184 GACGAGCAGTGCCAGCAGCTCCGCTCCGAGTACGTGGCGCAATGCCTGGGCCGGGGC----- 239
         |||||||||||||||||||| |||||||||||||||| ||| |||||||||||||
Db 106 GACGAGCGGGTGCCAGCAGCTCCGCTCTGAGTACGTGGCGCAATGCCTGGGCCGGCAGCG 165

Qy 240 -----GGGCTGGCGGGGGACCCGGGAGCTGCGTCGCTCCCCGGGCGCCTGCGCCGTCCCTCGC 294
               |||| ||||||||||||||||||||||||||||||||||||||||||||
Db 166 CCCGGGGGGCAGGGCCGGGGGGGGCCGGGGGGCGGGGGGCTCCCCGGGCGCCTGCGC 225

Qy 295 CGCTTCTTCCGCGCGGCCGCGGCGGGGGCTTCACGCACGCACGGGATCGGAA 354
         |||||| || ||||||||||||| || ||||||||| ||||| |||||
Db 226 CGCTTCTTCGCGCGGTGGGCTCGGCCCTCAGCGATGCGCTCTTCTCGCGGCGAA 285

```
Qy  355 GGCCCCGGGGTGCCGCGAGCGCGCGCAGACATTCGGCCGTGCCGTTCTCCGGC 414
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  286 GGCTCCGGCCTGCGCGGCCGAGGGCGCCAGACTTCGGCCGTGCCGTTCTCCGGC 345

Qy  415 CCCCAGCGTGGGCGGCCACCTTCCTGCCTGGAAGCCCTTGCGACGGAAGCCGCCGG 474
        ||||||||||| ||||||| |||||||||||||||||||||||||||||||||
Db  346 CCGGGGGTTGGGTGCGCGCCCCTTCTTCTTGCCTGGAAGCGCTGCGAGGGCAGCGCGCCTG 405

Qy  475 TGCCGGCGCCCCGTCTCTTTGCCTTCATGCCGTCATGCGGCTCCCGGGAC 534
        ||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  406 TGCCGGCGCCCCGTCTCCTTCGCTTCATGCGGCTCCCGGGAC 465

Qy  535 GGCTGGTGCCGGAGGAGGGGGGGGCCCCGGGGCCTGCTGGGCGTGCTTGTAGGCACC 594
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  466 CGGTGCCCGGAGGAGGGGGGCCCCGGTTGTTGTCTCGGAGGGCTCATAGGCGAC 525

Qy  595 GTGGTCACCCCAACTACCTGACAACGTGAGCGCCGGCGGGTTTGGGCCCTGGTGTCGGGCTGT 654
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  526 GTGGTCACCCCAACTACCTGACAACGTGAGCGCCGGCGGGTTTGGGCCCTGGTGTCGGGCTGT 585

Qy  655 GAGGCCAGCGGAAACGGGGGGAAGAGTGGGAAGCCTTCCGGCAGAGCTTTTTACAAGGAAC 714
        ||||||||||||||||||||
Db  586 GCGGCCAGTGGAAACCGGCGCGAAGAAGTCGGAAGCCTTCCGCAAGCTCTTTACACAAGGAAC 645

Qy  715 CCCTGCTTGGATGGTGTGCCATACAAGGCCCTTTGACAGCTCGCCAACCATCAGTTCTGCAGGAC 774
        ||||||||||||||||
Db  646 CCCTGCTTGGATGGTGTGCCATACAAGGCCTTTGACAGCTCGCCATCAGTTCTGCAGGAC 705

Qy  775 CAGTGGGAACCCCTACCAGAATGCTGGGCGAGGCCAAGGTGGGGCCTGACTGGGCTGAGA 834
        ||||||||||||||||
Db  706 CAG----------ACTGCTGGGGTGCTGTTTCCCCGCGGGCAAGGCACGAGTGGCCTGAGAA 755

Qy  835 GAGATGGAGGCAGAGAAAACGGTCCCCGGTTTTGT----------CCCAAGGTGTCCTCCGATGTCCA 887
        |||||||||
Db  756 GGACTGGAGGCAGAAACAGTCCTTGTTTTGTCCTAACGCCCCAAGGTGTCCTGGGCTGTATG 815

Qy  888 TACTCACTGCTTGCCCTCGGCCTTCTCCAGCCCCCTCTAATTAGGAAGAGGTGAACCATGGACAACA 947
        ||||||||||||||
Db  816 CACTCACTGCCCTGGCCTCTTCCAGCCGCCTCGATTAGGACAACATGAACCGTGGACGACA 875

Qy  948 CAGTGGA 954
        ||||||
Db  876 CAGTGA 882
```

RESULT 4

```
AAF57270

ID   AAF57270 standard; cDNA; 834 BP.
XX
AC   AAF57270;
XX
DT   29-MAY-2001 (first entry)
XX
DE   Mouse Ret5 polypeptide encoding cDNA.
XX
KW   Ret ligand 5; Ret5; autophosphorylation; tumour; renal; nephrotropic;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease; mouse;
KW   vulnerary; nootropic; anti-HIV; neuroprotective; antibacterial; ss;
KW   cerebroprotective; hemostatic; antiinflammatory; antiviral; neuroleptic.
XX
OS   Mus sp.
XX
PN   WO200116169-A2.
XX
PD   08-MAR-2001.
XX
PF   01-SEP-2000; 2000WO-US0024111.
XX
PR   01-SEP-1999; 99US-0152024P.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Worley D;
XX
DR   WPI; 2001-235091/24.
DR   P-PSDB; AAB62103.
XX
PT   Novel Ret ligand polypeptide useful for suppressing growth of a tumor
PT   cell that expresses Ret and for modulating Ret signal transduction
PT   involving a cell expressing Ret polypeptide.
XX
PS   Claim 1; Fig 1; 76pp; English.
XX
CC   The invention relates to mouse and human Ret ligand 5 (Ret5)
CC   polypeptides. The Ret5 polypeptides can be expressed by standard
CC   recombinant methodology. The Ret5 when bound to Ret, acts as a
CC   dimerization or autophosphorylation activator. The polypeptides and their
CC   antibodies are useful for stimulating growth of or limiting damage to,
CC   Ret expressing tissue in a subject, for suppressing growth of a tumour
CC   cell that expresses Ret, for modulating Ret signal transduction involving
CC   a cell expressing the Ret polypeptide. The Ret5 polypeptides, fusion
CC   proteins containing Ret5 and antibodies are useful for stimulating renal
CC   tissue growth and/or survival, supporting renal function and minimizing
CC   damage to renal tissue after various insults, particularly for treating
CC   acute renal failure, acute nephritis, chronic renal failure, nephrotic
CC   syndrome, renal tubule defects, kidney transplants, toxic injury, hypoxic
CC   injury and trauma. The compounds are also useful for treating conditions
CC   such as neural degeneration where neural growth and regeneration are
CC   desirable, e.g., Alzheimer's disease, Parkinson's disease, Huntington's
CC   disease, Tourette's syndrome, amyotrophic lateral sclerosis, as well as
CC   motor neuron disease, demyelinating disease, bacterial diseases, viral
CC   diseases, and prion diseases including Creutzfeldt-Jakob disease. The
CC   compounds are also useful for treating disorders due to damage to neural
CC   tissue caused by neoplastic impingement, trauma or cerebrovascular events
CC   such as hemorrhage or emboli, and neural disorders such as mental
CC   retardation, autism, fetal alcohol syndrome, Down's syndrome and cerebral
CC   palsy. The present sequence represents the mouse Ret5 cDNA sequence
CC   predicted by visual inspection method
XX
SQ   Sequence 834 BP; 110 A; 291 C; 281 G; 152 T; 0 U; 0 Other;
```

```
Query Match             58.7%;  Score 591.8;  DB 4;  Length 834;
Best Local Similarity   87.2%;
Matches  711;  Conservative  0;  Mismatches  62;  Indels  42;  Gaps  4;

Qy  124 GGGTCAGCGAGCTCCACTGAGGGGAAATCCGTCGGTGGAGAGCGCGTGCACAGCA 183
        |||||||||||||||||||||||||||||||||||||||||||||||
Db   46 GGGGTCTGCGAGCTTTACCGACGGAGAATCCGTCGGTGGAGACGGCGGTGTACAGCA 105

Qy  184 GACGGACAGTGCCAGCAGCTCGCGCGCTCCGAGTACTACGTGGCGCCAATGCCTGGGCCGGGC--- 239
        ||||||||||||||||||||||||||
Db  106 GACGAGCGGTGCCAGCAGTGTGCGCTTCGAGTACCGTGGCGCACGATGCCTGGCGCCGGGCAGCG 165

Qy  240 -----GGGCTGGCGGGGACCCGGAGCTGGCGTGCGGTGCGCGCTCCCGCGGCCGTGCCCGC 294
        |||||||||||||||||||||||||||
Db  166 CCCCGGGGGCGCAGGCCCGGGACCCGGGAGGCTCGGTGGCCTCGCCCGCCGCCGGATGCGGA 225

Qy  295 CGCTTCTTCGCCCCGGGGCCTCACGCACGCGCCGCTCTTCTTCTGCGGATGCGAA 354
        |||||||||||||||||||||||
Db  226 CGCTTCTTCGCCGGCCGTGTGGGCGCTCCGGGCGCCTCCGCTCTTCTTCTCGCGGA 285

Qy  355 GGCCCCGGCGTGCCGCGAGCGCGCGCAGACATTCGGCCGTGCCGTTCTCCGGC 414
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  286 GGCTCCGGCCTGCGCGGCCGAGGGCGCCAGACTTCGGCCGTGCCGTTCTCCGGC 345

Qy  415 CCCCAGCTGGCGCGCCACCTTCCTGCCTGGAAGCCCTTGGACGGAAGCCGCCGG 474
        |||||||||||||||||||||||||
Db  345 
```

RESULT 5

```
AAF57273

ID   AAF57273 standard; cDNA; 783 BP.
XX
AC   AAF57273;
XX
DT   29-MAY-2001  (first entry)
XX
DE   Mouse Ret15 alternatively spliced polypeptide encoding cDNA.
XX
KW   Ret ligand 5; Ret15; autophosphorylation; tumour; renal; nephrotropic;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease; mouse;
KW   vulnerary; nootropic; anti-HIV; neuroprotective; antibacterial; ss;
KW   cerebroprotective; hemostatic; antiinflammatory; antiviral; neuroleptic.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..783
FT                   /*tag= a
FT                   /product= "alternatively spliced Ret15"
XX
PN   WO200116169-A2.
XX
PD   08-MAR-2001.
XX
PF   01-SEP-2000; 2000WO-US024111.
XX
PR   01-SEP-1999; 99US-0152024P.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Worley D;
XX
DR   WPI; 2001-235091/24.
DR   P-PSDB; AAB62106.
XX
PT   Novel Ret ligand polypeptide useful for suppressing growth of a tumor
PT   cell that expresses Ret and for modulating Ret signal transduction
PT   involving a cell expressing Ret polypeptide or Ret ligand polypeptide.
XX
PS   Disclosure; Fig 7; 76pp; English.
XX
CC   The invention relates to mouse and human Ret ligand 5 (Ret15)
CC   polypeptides. The Ret15 polypeptides can be expressed by standard
CC   recombinant methodology. The Ret15 polypeptides when bound to Ret, acts as a
CC   dimerization or autophosphorylation activator. The polypeptides and their
CC   antibodies are useful for stimulating growth of or limiting damage to,
CC   Ret expressing tissue in a subject, for suppressing growth of a tumour
CC   cell that expresses Ret, for modulating Ret signal transduction involving
CC   a cell expressing the Ret polypeptide. The Ret15 polypeptides, fusion
CC   proteins containing Ret15 and antibodies are useful for stimulating renal
CC   tissue growth and/or survival, supporting renal function and minimizing
CC   damage to renal tissue after various insults, particularly for treating
CC   acute renal failure, acute nephritis, chronic renal failure, nephrotic
CC   syndrome, renal tubule defects, kidney transplants, toxic injury, hypoxic
CC   injury and trauma. The compounds are also useful for treating conditions
CC   such as neural degeneration where neural growth and regeneration are
CC   desirable, e.g., Alzheimer's disease, Parkinson's disease, Huntington's
CC   disease, Tourette's syndrome, amyotrophic lateral sclerosis, as well as
CC   motor neuron disease, demyelinating disease, bacterial diseases, viral
CC   diseases, and prion diseases including Creutzfeldt-Jakob disease. The
CC   compounds are also useful for treating disorders due to damage to neural
CC   tissue caused by neoplastic impingement, trauma or cerebrovascular events
CC   such as hemorrhage or emboli, and neural disorders such as mental
CC   retardation, autism, fetal alcohol syndrome, Down's syndrome and cerebral
CC   palsy. The present sequence represents an alternatively spliced mouse
CC   Ret15 encoding cDNA.
XX
SQ   Sequence 783 BP; 92 A; 280 C; 266 G; 145 T; 0 U; 0 Other;
```

Query Match 55.4%; Score 558.2; DB 4; Length 783;
Best Local Similarity 91.4%; Pred. No. 2.1e-109;
Matches 606; Conservative 0; Mismatches 48; Indels 9; Gaps 1;

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Qy   124 GACGAGCAGTGCCAGCAGCTGCCTCCGAGTACGTGCGCAATGCCTGGGCGCCGGGC----- 183
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Db    46 GGGGTCTGCGAGCTTTACCGACGGGAATCGCTTGCGTGGACGCCGGGAGCGGGTGTACAGCA 105

Qy   184 GACGAGCAGTGCCAGCAGCTGCCTCCGAGTACGTGCGCAATGCCTGGGCGCCGGGC----- 239
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   106 GACGAGCAGTGCCAGCAGCTGCCTCTGAGTACGTGCGCACGATGCCTGGGCGCCCAGCG 165

Qy   240 -----GGGCTGGCGGGGACCCGGGGAGCTGGCGTCGCCTGGCCTCCCGGGCGTGCCCTGCGC 294
              ||||||||||| ||||| | |||| |||||| |||| ||||| |||| ||
Db   166 CCCGGGGGCAGGCGGGGGACCCGGGGGCTGGCGTGGCGTCCCGGCTCGCGC 225

Qy   295 CGCTTCTTCGCCCCGGGCGGGGCCCTCGGGCCTCAGGCACGCGTCGCTCTTCTTCGTGCGGATGCGAA 354
         ||| |||| || | |||| | ||| | |||| |||||| |||| | | | |||||||
Db   226 CGCTTCTTCGCCCGGTGGGCCTCCGGGGCCTCAGGCATGCGTCGCTTCTTCGTGCGGGATGCGGA 285

Qy   355 GGCCCCGGCCGTGCGCTGGGCCCAGACAATTCGCGCCCGGGTTCTCCGGC 414
         ||||| || |||||||||||||||| | ||| |||||||| |||||||
Db   286 GGCTCCGGTGCGCCCGGAGCGCGCCGGACTTTCGCGCCCGCGGTTCTCGGC 345

Qy   415 CCCCAGCTGGCGGCCACCTTCCTCGCCTGGAAGCCCTTGGAGCGGGAGCCGCCGCCGG 474
         ||||| ||||||| | ||||| | ||||| |||||| |||||||| |||| |||
Db   346 CCGGGGGTTGGTGCCGCCCTCTTCGGCCTGGAGCCCCTGGCGCGCCGGGCTG 405

Qy   475 TGCCGGGCGCCCCGGTCTCTTTGCCTTCCAGGCCTCATGCCCCTCCCGGAC 534
         ||||| |||||| |||| ||| |||||||||||||| || |||||||
Db   406 TGCCGGGCGCCCCGGTCTCCTTGCCTTCCAGGCCTCATGCGGCTCCCGGAC 465

Qy   535 GGCTGTCCGGAGGAGGAGGGGGGGCCCCGGGCGTGTCGGCTGT 594
         |||| |||||||||||||||||||||||| ||||| ||
Db   466 CGCTGCCCGGAGGAGGGGGGGGCCGGGTTGTCGCGCTTAGGCACC 525

Qy   595 GTGGGTCACCCCCAACTACCTGGACAACGTGAGGCGGCGCCTGT 654
         |||| ||||| || |||||| ||||||| || |||||
Db   526 GTGGGTCACCCCCAACTACCTGGACAACGTGAGGCGGCGCCTGT 585
```

```
Qy   655  GAGGCCAGGGAAACCGGGCCGGAAGAGTGCGAAGCTTCCGCAAGCTTTTTACAAGGAAC  714
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   586  GCCGGCCAGTGGGAAACCGGGCGCGGAAGAATGCGAAGCCTTCCGCAAGCTCTTTACAAGGAAC  645

Qy   715  CCCTGCTTGGATGGTGCCATACAACAGCCTTTGACAGCTCGGAACCATCAGTTCTCGCAGGAC  774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   646  CCCTGCTTGGATGGTGCCATACAAGCCTTTGACAGCTCGGAACCATCAGTTCTCCGAGGAC  705

Qy   775  CAG  777
              |||
Db   706  CAG  708
```

RESULT 6

```
ID   ABL51669    standard;  cDNA;  783 BP.
XX
AC   ABL51669;
XX
DT   08-JUL-2002  (first entry)
XX
DE   Mouse GPI-anchored isoform a1 encoding cDNA SEQ ID NO:7.
XX
KW   GFRalpha4;  glycosyl-phosphatidylinositol;  GPI;  GDNF;  cytostatic;
KW   glycosyl-phosphatidylinositol-linked GDNF family alpha-receptor;
KW   glial cell line derived neurotrophic factor; osteopathic; tumour;
KW   neuroprotective; anticonvulsant; neoplasia; endocrine tumour;
KW   medullary thyroid carcinoma; pheochromocytoma; parathyroid hyperplasia;
KW   neuronal disorder; aberrant axonal sprouting; gene; ss.
XX
OS   Mus musculus.
XX
FH   Key               Location/Qualifiers
FT   CDS               1..783
FT                     /*tag= a
FT                     /product= "GPI-anchored isoform a1"
XX
XX
PN   WO200162795-A1.
XX
PD   30-AUG-2001.
XX
PF   14-NOV-2000;  2000WO-FI000994.
XX
PR   21-FEB-2000;  2000FI-00000394.
XX
PA   (LICE-) LICENTIA LTD.
XX
PI   Airaksinen M,  Saarma M,  Poteriaev D,  Lindahl M,  Timmusk T;
PI   Rossi J;
XX
DR   WPI; 2001-596722/67.
DR   P-PSDB; ABB09214.
XX
PT   New nucleic acid sequence for manufacturing polypeptides for treating
PT   endocrine cancers comprises a cDNA encoding a splicing isoform of
PT   mammalian growth factor receptor (GFR)alpha4.
XX
PS   Claim 4; Fig 18A; 143pp; English.
XX
CC   The present invention describes an isolated and purified cDNA sequence
CC   encoding a splicing isoform of a mammalian growth factor receptor
CC   (GFR)alpha4, or its fragments. GFRalpha4 sequences have cytostatic,
CC   osteopathic, neuroprotective and anticonvulsant activities. GFRalpha4 is
CC   a glycosyl-phosphatidylinositol (GPI)-linked glial cell line-derived
CC   neurotrophic factor (GDNF) family alpha-receptor. A GFRalpha4
CC   polynucleotide sequence can be used for recording GFRalpha4 mediated
CC   signaling in neurons or endocrine cells such as thyroid calcitonin-
CC   producing C-cells, parathyroid gland cells, adrenal chromaffin cells, or
CC   cells from the pituitary intermediate lobe. GFRalpha4 protein and
CC   polynucleotide sequences can are used for manufacturing polypeptides
CC   useful for diagnosing and/or treating tumours in parathyroid gland cells,
CC   adrenal chromaffin cells, cells of pituitary intermediate lobe,
CC   neoplasia, endocrine tumours, medullary thyroid carcinoma and
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(second column)

```
CC   pheochromocytoma, parathyroid hyperplasia, neuronal disorders or for
CC   preventing neuronal death or aberrant axonal sprouting. The present
CC   sequence encodes the mouse GFRalpha 4 protein, designated GPI-anchored
CC   isoform a1, from the present invention
XX
SQ   Sequence 783 BP; 92 A; 280 C; 266 G; 145 T; 0 U; 0 Other;

Query Match             55.4%;  Score 558.2;  DB 4;  Length 783;
Best Local Similarity   91.4%;  Pred. No. 2.1e-109;
Matches  606;  Conservative  0;  Mismatches  48;  Indels  9;  Gaps  1;

Qy   124  GGGTCAGGCCAGAGCTCCCACTGAGGGGAAATCGCTGCCTGGACGCACAGCGGGTGTACAGCA  183
              ||| ||  |  ||||  ||||| ||||| ||||  ||||||||| |||  | || |||
Db   46   GGGGTCTGCGCAGGCTTTACCGACGCGGAAATCCGTCGCCTGGACGGGGCGGGTGTACAGCA  105

Qy   184  GACGAGCAGTGCCAGCACAGTGTGCGTCCGAGCTAGCACGTGGCGGACGGGCGCCCTGCGC  239
              ||||||||||||||||||  |||||||||||||||  |||||||||| |||||||||||
Db   106  GACGAGCGGTGCCAGCACAGTGTGCGCTCCGAGTACGTGGCGACGGGCGCCCTGCGC  165

Qy   240  -----GGGCTGGCGGGGGACCCGGGAGCTCGGTGCCGTGCGGGCCGGCCCGGGCCGCTGCGC  294
                   |||||||||||| |||| | ||| ||||| || |||||||| || ||||||||
Db   106  CCCGGGGCGCAGGCGCCGGGACCCGGGAGCTCGGTGCCGTGCGGGCCGGCCCGGGCCGCTGCGC  165

Qy   295  CGCTTCTTTGGCCCGCGGGGCCTCCGGCGCGCTCACCGCACGCGCTCTCTTCTGCGGATGCGAA  354
              |||||  |||| ||||||||||||||||| |||||| |||||  || || ||||| |||
Db   226  CGCTTCTTTCCGCCGTGGGCCTTCACGCTCACCGCATGGCGCTCTCTTCTCCGGGCTGCGAA  285

Qy   355  GGCCCCGCGTGGCCGCGAGCCCGCCCAGACAATTCGCGCCGGCGCGGGCCGGTTCTCCGGC  414
              |||||||||| ||||||||| ||||||| ||||||||| ||||||| ||||| ||||||
Db   286  GGCTCCGGCGTGGCCGCGAGGCCGCCCAGACTTTCGCGGCGGGCCGGTTCTCCGGC  345

Qy   415  CCCCAAGCTGCGCGCCACCTTCCTGCCTGAAGCCCTTGGACGGCGCTGCCGAGGGCCGCGG  474
              |||| ||||||| |||||| | |||||||||| ||||||||| || || |||||| |||||
Db   346  CCGGGGGTTGGTCGCCCGCTTCTTGGCCCTTGGAGCCCCTGGGGAGCGCCCGCCCTG  405

Qy   475  TGCCGGGGCCCCGGCCCTTGCTTCTTTGCCTTCCCAGGCGCTCCTCCATGGCTCATCCGCCCGGGCGCTGCC  534
              |||||||||||| |||||| ||| |||||||||| ||||| ||||||||||| |||| |||| |||
Db   346  CCGGGGGTTGGTCGCCCGCTTCTTGGCCCTTGGAGCCCCTGGGGAGCGCCCGCCCTG  405

Qy   535  GGCTGTCCGGGAGGAGGAGGGGGGGCCGGCCGTGTCTGCGGCCCTTACGCAGCGGGTTGTAGGCACC  594
              |||||| |||||||| ||||||| |||||||||| || ||  |||||||||||||| ||||||||
Db   466  CGCTGCCCCGGAGGAGGGGGGCCCCGGTTGTCTCGCGGCGGCCTTACGCAGGCCTCATAGGCACC  525

Qy   595  GTGGTCACCCCCAACTACCTGGACAACGTGAGCGCGGCGGGCCCCTGTGCCGCCCTGTGCGGCTGT  654
              |||||||||||||||||||||||||||  |||||||||||||||||||||| |||||| ||||||
Db   526  GTGGTCACCCCCAACTACCTGGACAACGTGAGCGCGGCGGGCCCCTGTGCCGCCCTGTGCGGCTGT  585

Qy   655  GAGGCCAGGGAAACCGGGCCGGAAGAGTGCGAAGCTTCCGCAAGCTTTTTACAAGGAAC  714
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   646  GCCGGCCAGTGGGAAACCGGGCGCGGAAGAATGCGAAGCCTTCCGCAAGCTCTTTACAAGGAAC  645

Qy   715  CCCTGCTTGGATGGTGCCATACAACAGCCTTTGACAGCTCGGAACCATCAGTTCTCGCAGGAC  774
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db   646  CCCTGCTTGGATGGTGCCATACAAGCCTTTGACAGCTCGGAACCATCAGTTCTCCGAGGAC  705

Qy   775  CAG  777
              |||
Db   706  CAG  708
```

RESULT 7

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ID   AAF57271    standard;  cDNA;  795 BP.
XX
AC   AAF57271;
XX
DT   29-MAY-2001  (first entry)
XX
DE   Mouse Ret5 polypeptide encoding cDNA.
XX
KW   Ret ligand 5; Ret5;  autophosphorylation;  tumour;  renal;  nephrotropic;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease; mouse;
KW   vulnerary; nootropic; anti-HIV; neuroprotective; antibacterial; ss;
```

```
KW   cerebroprotective; hemostatic; antiinflammatory; antiviral; neuroleptic.
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..795
FT                   /*tag= a
FT                   /product= "Ret15"
FT   sig_peptide     1..63
FT                   /*tag= b
FT   mat_peptide     64..792
FT                   /*tag= c
XX
PN   WO200116169-A2.
XX
PD   08-MAR-2001.
XX
PF   01-SEP-2000; 2000WO-US024111.
DR   WPI; 2001-235091/24.
DR   P-PSDB; AAB62104.
XX
PR   01-SEP-1999; 99US-0152024P.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Worley D;
XX
PT   The invention relates to mouse and human Ret ligand 5 (Ret15)
     polypeptides. The Ret15 polypeptides can be expressed by standard
     recombinant methodology. The Ret15 polypeptides and their
     antibodies are useful for stimulating growth of a tumour
     cell that expresses Ret, for suppressing growth of a tumour
     cell expressing the Ret polypeptide. The Ret15 polypeptides, fusion
     proteins containing Ret15 and antibodies are useful for stimulating renal
     tissue growth and/or survival, supporting renal function and minimizing
     damage to renal tissue after various insults, particularly for treating
     acute renal failure, acute nephritis, chronic renal failure, nephrotic
     syndrome, renal tubule defects, kidney transplants, toxic injury, hypoxic
     injury and trauma. The compounds are also useful for treating conditions
     such as neural degeneration where neural growth and regeneration are
     desirable, e.g., Alzheimer's disease, Parkinson's disease, Huntington's
     disease, Tourette's syndrome, amyotrophic lateral sclerosis, as well as
     motor neuron disease, demyelinating disease, bacterial diseases, viral
     diseases, and prion diseases including Creutzfeldt-Jakob disease. The
     compounds are also useful for treating disorders due to damage to neural
     tissue caused by neoplastic impingement, trauma or cerebrovascular events
     such as hemorrhage or emboli, and neural disorders such as mental
     retardation, autism, fetal alcohol syndrome, Down's syndrome and cerebral
     palsy. The present sequence represents the mouse Ret15 cDNA sequence
     predicted from DSW300 sequence by GENESCAN/GENE ALEX
PS   Claim 1; Fig 2; 76pp; English.
```

The invention relates to mouse and human Ret ligand 5 (Ret15)
polypeptides. ...

Novel Ret ligand polypeptide useful for suppressing growth of a tumor
cell that expresses Ret and for modulating Ret signal transduction
involving a cell expressing Ret polypeptide or Ret ligand polypeptide.

The polypeptides and their antibodies are useful for stimulating growth of a tumour
cell expressing tissue in a subject, for suppressing growth of a tumour
cell that expresses Ret, for modulating Ret signal transduction involving
a cell expressing the Ret polypeptide. The Ret15 polypeptides,
dimerization or autophosphorylation activator. The polypeptides and their

```
SQ   Sequence 795 BP; 94 A; 271 C; 282 G; 148 T; 0 U; 0 Other;

Query Match        50.7%;  Score 510.6;  DB 4;  Length 795;
Best Local Similarity   88.5%;
Matches  587;  Conservative    0;  Mismatches  49;  Indels   27;  Gaps    2;
Pred. No. 2.9e-99;

Qy  124 GGGGTCAGCGAGCTCCACTGAGGGGGAATCGTTGCGTGGAAGCAGCCCAGGCGCTGCACAGCA 183
        ||||||| ||||||||||||||||||||||||||||| || | ||||||| |||||||||||||
Db   46 GGGGTCTGCGAGCTTTACCGACCGGGAANTCGCTCCGTGGACGCGGCGTGTACAGCA 105

Qy  184 GACGAGGCAGTGCCAGCGAGCTGGGCTGCGCTCCGAGTACGTGGCGCAATGCCTGGGGCCCGGGG----- 239
        ||||||| |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db  106 GACGAGCGGTGCCAGCAGCTGGGCTCAGATGCCTGAGTACGTACGTGGCACGAGTGCCTGGGGCCCGGCAGCG 165
```

```
RESULT 8
AAZ28259
ID   AAZ28259 standard; cDNA; 1019 BP.
XX
AC   AAZ28259;
XX
DT   05-JAN-2000  (first entry)
XX
DE   Murine glial derived neurotrophic factor receptor-alpha-X cDNA.
XX
KW   Glial derived neurotrophic factor-alpha-X; GFR-alpha-X; neural cell;
KW   survival; function; nervous system; signalling; diagnosis; treatment;
KW   neurological disorder; sensory disorder; Dejerine-Roussy syndrome;
KW   contralateral anaesthesia; eating disorder; obesity; motor disorder;
KW   Parkinson's disease; amyotrophic lateral sclerosis; ALS;
KW   cognitive disorder; Alzheimer's disease; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1019
FT                   /*tag= a
FT                   /product= "Murine GFR-alpha-X protein"
FT                   /note= "No initiation or termination codons given in
FT                   specification"
FT                   /transl_except= (pos:601..603, aa:Xaa)
FT                   /note= "Xaa = unknown"
FT                   /transl_except= (pos:649..651, aa:Xaa)
FT                   /note= "Xaa = unknown"
FT                   /transl_except= (pos:1018..1019, aa:Xaa)
FT                   /note= "Xaa = unknown"
```

XX
PN WO9950298-A1.
XX
PD 07-OCT-1999.
XX
PF 25-MAR-1999; 99WO-US006631.
XX
PR 31-MAR-1998; 98US-0080070P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Moore KJ;
XX
DR WPI; 1999-591276/50.
DR P-PSDB; AAY42771.
XX

Claim 7; Fig 1; 100pp; English.

PT A nucleic acid molecule that encodes GDNF Family Receptor alpha-X
PT protein, methods of isolation and antibodies - useful for the detection
PT of homologues and identification of binding compounds.
XX

CC This sequence represents murine glial derived neurotrophic factor
CC receptor-alpha-X (GFR-alpha-X) cDNA. GFR-alpha-X is a fourth member of
CC the glial derived neurotrophic (GFR-alpha) family of receptors. The cDNA
CC was identified in a positional cloning process in which the mouse
CC mahogany locus was being sequenced to identify genes involved in obesity.
CC The GFR-alpha-X protein binds to neurotrophic factors such as GDNF (glial
CC cell line-derived neurotrophic factor) and/or NTN (neurturin), and
CC mediates signalling within cells expressing the GFR-alpha-X protein. GFR-
CC alpha-X, like the other three member of the GFR-alpha family (GFR-alpha-
CC 1, -2, and -3), transmits a signal to the interior of a cell by
CC activation of the RET protein tyrosine kinase signaling pathway.
CC Neurotrophic factors promote survival and function of neural cells of
CC both the central and peripheral nervous systems. Modulation of GFR-alpha-
CC X activity can result in modulation of the neurotrophic factor- initiated
CC cell function. Probes and/or primers derived from GFR-alpha-X cDNA, and
CC antibodies against the protein are used to detect the presence of GFR-
CC alpha-X nucleic acids or protein and can be used in the diagnosis and
CC treatment of a variety of neurological disorders, including sensory
CC disorders (e.g., Dejerine-Roussy syndrome, contralateral anaesthesia, and
CC certain eating disorders), motor disorders (e.g., Parkinson's disease,
CC amyotrophic lateral sclerosis), and cognitive disorders (e.g.,
CC Alzheimer's disease). In addition, compounds which bind to GFR-alpha-x
CC may be used to modulate the activity of the protein
XX
SQ Sequence 1019 BP; 148 A; 340 C; 343 G; 186 T; 0 U; 2 Other;

Query Match   48.3%; Score 487.2; DB 2; Length 1019;
Best Local Similarity   90.4%; Pred. No. 2.9e-94;
Matches 557; Conservative   0; Mismatches   48; Indels   11; Gaps   3;

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Qy   123 AGGGTCAGCGAGCTCCACTGAGGAGGGAATCGGTCGCTGCGTGGAAGCAGCGCGAGGCGTGCACAGC 182
         ||||||||| ||| || |||||||||||| |||||||||||||| |||||| ||||||||||||
Db    54 AGGGTCTGCGAGCTTTACCGACGGAATCCCTCGGCCGCCGAGCCGTGTACAGC 113

Qy   183 AGACAGCAGTGCCAGCTGCGCTCCCAGTACGTGGGCCCAATCCCTGGGCCCGGGC--- 239
         |||||||||||| |||||| ||||||||||| ||||||| ||||||||||||
Db   114 AGACGAGCGGGTGCCACCAGCTGCGCTCTGACTACGTGGCACGATGCCTGGGCCGGCAGC 173

Qy   240 -----GGGCTGGGCGGGGGACCCGGAGCTCGGTCGCCCTGCCCCTGCG 293
              |||||||| ||||| ||||||| ||||| |||||||||
Db   174 GCCCGGGGGGGCAGGCGCGGGACCCGGGCTCGGGTCCCCGCTGTCCGCGGATGCGA 233

Qy   294 CCGCTTCTTCCCCCGGGGGGCCTCCGGCGCTCACGCACGCAGGCGGGATGCGGA 353
         |||| ||| ||||| || ||||| |||||||||  |||||||| |||
Db   234 CCGCTTCTTCCGGCGTGGGGGCTCTGGGTTGCCGCTGCTCTTCTCGGCGGCGGA 293

Qy   354 AGGGCCCGGGCGGCGTGCGCGCGGAGGCCCCGGGCCGCGGGCGGGTTCTCGG 413
         ||||||||| ||||| ||||||||||||||| ||||||||| |||||||
Db   294 AGGGCTCCGGCGGTGCGCCGGAGCGGCCGCCCAGACTTTCGCGGCGGTTCTCCGG 353

Qy   414 CCCCCAGCTGGCCGCACCTTCCTGCCTGGACGCCTGGCGAGCGAAGCGCCCG 473
```

RESULT 9
AAF31061

ID AAF31061 standard; DNA; 2522 BP.
XX
AC AAF31061;
XX
DT 06-APR-2001 (first entry)
XX
DE Rat GFRalpha-4 gene.
XX
KW Rat; GFRalpha-4; carcinoma; familial hirschsprung disease; pain;
KW glial cell-line derived neurotrophic factor; neurodegenerative disease;
KW GDNF family receptor alpha-4; Alzheimer's disease; Parkinson's disease;
KW motor neuron disease; peripheral neuropathy; spinal cord injury;
KW chromosome 3q36; ds.
XX
OS Rattus rattus.
XX
PN WO20010102557-A1.
XX
PD 11-JAN-2001.
XX
PF 26-MAY-2000; 2000WO-EP004918.
XX
PR 29-JUN-1999; 99GB-00015200.
XX
PA (JANC) JANSSEN PHARM NV.
XX
PI Masure SLJ, Cik M, Hoefnagel EW;
XX
DR WPI; 2001-138137/14.
DR P-PSDB; AAB61636, AAB61637.
XX
PT Glial cell-line derived neurotrophic factor family receptor alpha-4,
PT useful for preparing medicaments for treating neurodegenerative diseases
PT (e.g. Alzheimer's disease, Parkinson's disease) and carcinomas.
XX
PS Claim 6; Page 71-72; 82pp; English.
XX
CC The present invention relates to rat Glial cell-line Derived Neurotrophic
CC Factor (GDNF) family receptor alpha-4 (GFRalpha-4; see AAB61636 and
CC AAB61637). The present sequence is the rat GFRalpha-4 gene. GFRalpha-4 is
CC useful in the preparation of a medicament for the treatment of
CC neurodegenerative diseases, Alzheimer's disease, Parkinson's disease,
CC motor neuron disease, peripheral neuropathy, spinal cord injury, familial
CC hirschsprung disease, carcinomas, and diseases associated with GFRalpha-4
CC receptor dysfunction and in alleviating pain. The rat GFRalpha-4 gene is
CC localised on chromosome 3q36

```
Db   354 CCCGGGGGTTGGGTGCGGCGCCCCCTTCGCCTGGCTGGCGCCCCTGGAGCCGGCTGTGCGAGGCGGCAGGCGGCCT 413

Qy   474 GTGCGCGGCGCCGCCCGTCGCTCTTTGCCTTCTTCAGCGTCCAGCCTGGGC 533
Db   414 GTGCCGCGGCCCGTCTTCCTTGCCTTCCAGCGCCATGCGGGCTCCATGCGGCTCCCCGGA 473

Qy   534 CGGGCTGTCCGGAGGAGGGGGGCCCCGGCCGTCGCGGCCTACGCAGGCGCTTGTGAGGCAC 593
Db   474 CCGCTGCCCGGAGGAGGGGGCGCCCCCGGCGTTGTCTCGGCGGTCTAGCAGGCGCCATAGGCAC 533

Qy   594 CGTGGTTCACCCCCCAACTACCTTGGACAACGTGAGGCGGCGCGGGTTCGGCGGCCCTGCG 653
Db   534 CGTGGTTCACCCCCAACTACCTGGGACAACGTGGGCGGCGCGGGTTGGCGGCCCTGGGTGCGGCTG 593

Qy   654 TGAGGCCA-GCGGAAACCCGGCGCGAAGAGTGCGGAGGCCTTCCCGCGCAGCGTTTTACAA-GG 711
Db   594 TGCGGCCANGTGGAAACCGGCGCGGCAAGAATGCGAAGCCTTCCCGCGCAAGCTTCTTTACAANGG 653

Qy   712 AACCCCTGCTTGGGTG 727
Db   654 AACCCCTGCTTGGGTG 669
```

XX

RESULT 10

ABL51672

ID   ABL51672 standard; cDNA; 810 BP.
XX
AC   ABL51672;
XX
DT   08-JUL-2002 (first entry)
XX
DE   Human GPI-anchored isoform a encoding cDNA SEQ ID NO:10.
XX
KW   GFRalpha4; glycosyl-phosphatidylinositol; GPI; GDNF; cytostatic;
KW   glycosyl-phosphatidylinositol-linked GDNF family alpha-receptor;
KW   glial cell line derived neurotrophic factor; osteopathic; tumour;
KW   neuroprotective; anticonvulsant; neoplasia; endocrine tumour;
KW   medullary thyroid carcinoma; pheochromocytoma; parathyroid hyperplasia;
KW   neuronal disorder; aberrant axonal sprouting; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT
FT   CDS   1..810
FT   /tag= a
FT   /product= "GPI-anchored isoform a"
XX
PN   WO20016279S-A1.
XX
PD   30-AUG-2001.
XX
PF   14-NOV-2000; 2000WO-FI000994.
XX
PR   21-FEB-2000; 2000FI-00000394.
XX
PA   (LICE-) LICENTIA LTD.
XX
PI   Airaksinen M, Saarma M, Poteriaev D, Lindahl M, Timmusk T;
PI   Rossi J;
XX
DR   WPI; 2001-596722/67.
DR   P-PSDB; ABB09217.
XX
PT   New nucleic acid sequence for manufacturing polypeptides for treating
PT   endocrine cancers comprises a cDNA encoding a splicing isoform of
PT   mammalian growth factor receptor (GFR)alpha4.
XX
PS   Claim 4; Fig 21A; 143pp; English.
XX
CC   The present invention describes an isolated and purified cDNA sequence
CC   encoding a splicing isoform of a mammalian growth factor receptor
CC   (GFR)alpha4, or its fragments. GFRalpha4 sequences have cytostatic,
CC   osteopathic, neuroprotective and anticonvulsant activities. GFRalpha4 is
CC   a glycosyl-phosphatidylinositol (GPI)-linked glial cell line-derived
CC   neurotrophic factor (GDNF) family alpha-receptor. A GFRalpha4
CC   polynucleotide sequence can be used for recording GFRalpha4 mediated
CC   signalling in neurons or endocrine cells such as thyroid calcitonin-
CC   producing C-cells, parathyroid gland cells, adrenal chromaffin cells, or
CC   cells from the pituitary intermediate lobe. GFRalpha4 protein and
CC   polynucleotide sequences can be are used for manufacturing polypeptides
CC   useful for diagnosing and/or treating tumours in parathyroid gland cells,
CC   adrenal chromaffin cells, cells of pituitary intermediate lobe.
CC   neoplasia, endocrine tumours, medullary thyroid carcinoma and
CC   pheochromocytoma, parathyroid hyperplasia, neuronal disorders or for
CC   preventing neuronal death or aberrant axonal sprouting. The present
CC   sequence encodes the human GFRalpha 4 protein, designated GPI-anchored
CC   isoform a, from the present invention
XX
SQ   Sequence 810 BP; 85 A; 314 C; 273 G; 138 T; 0 U; 0 Other;

Query Match   42.4%; Score 427.6; DB 4; Length 810;
Best Local Similarity 77.2%; Pred. No. 1.4e-81;
Matches 536; Conservative 0; Mismatches 149; Indels 9; Gaps 1;

Qy   124 GGGTCAGCCAGCTCCACTGAGGGGAATCGCTGGCGTGGAAGCAGCCGAGGCGTTGCACGCA 183
          ||| | |||| ||| | | || |||||| | |||||| |||| ||||||||||||||
Db   46 GGGTCCGGCGAGCTCGGTCGGAGGAACCGATGTGTGGACGGCGCGCGAAGCCTTGCACGCG 105

Qy   184 GACGAGAGAGTGCCAGCAGCTGGCGTCCAGTACGTACGTGCGCAATGCGTCGGGCGCGGCC 243
          |||||| | || ||||||||||| || || ||| |||||| ||||||| |||||
Db   106 GACGCGGCGGTGCCAGCGCGTTTGCGCTCCGAGTATGTGGGCGCAGTGCCTGGCGGGGC-- 161

Qy   244 TGGCGGGGGACCCGGGAGCTGCGTGCGGCCTCCCCGTCGCCGCCGCGCGCGCCGTTCTTC 303
          |||| || | ||||||||||| | | | || ||||||||||||| || ||||||||
Db   162 -----TGCGCAGGGGCGGGCGCTGGTGTCCCGGCGCCGCCCGCGCGCCCCTGCGCCTTCTTC 216

Qy   304 GCCCGCGGGGGGCGGGCTTCCCGCGGCGCTCACGCACCACGCGCTGCCTCTCTCGGGATGCGGAAGCC 363
          ||||||||||| |||| ||| |||| || || ||||| ||||||| || | |||| ||||||
Db   217 GCCCGCGGGGGGCCCCGGGCTCACCCAGCACTGCTTCTTCTGCCCGTCGCGGTGCGGCCCGCGGCG 276

RESULT 11
AAF57272

ID   AAF57272 standard; cDNA; 849 BP.
XX
AC   AAF57272;
XX
DT   29-MAY-2001 (first entry)
XX
DE   Human Ret15 polypeptide encoding cDNA.
XX
KW   Ret ligand 5; Ret15; autophosphorylation; tumour; renal; nephrotropic;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease; human;
KW   vulnerary; nootropic; anti-HIV; neuroprotective; antibacterial; ss;
KW   cerebroprotective; hemostatic; antiinflammatory; antiviral; neuroleptic.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..849
FT   /*tag= a
FT   /product= "Ret15"
FT   sig_peptide   1..60
FT   /*tag= b
FT   mat_peptide   61..846
FT   /*tag= c
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PN   WO200116169-A2.
PD   08-MAR-2001.
PF   01-SEP-2000; 2000WO-US024111.
PR   01-SEP-1999; 99US-0152024P.
PA   (BIOJ) BIOGEN INC.
PI   Worley D;
XX
DR   WPI; 2001-235091/24.
DR   P-PSDB; AAB62105.

PT   Novel Ret ligand polypeptide useful for suppressing growth of a tumor
PT   cell that expresses Ret and for modulating Ret signal transduction
PT   involving a cell expressing Ret polypeptide or Ret ligand polypeptide.
XX
PS   Claim 1; Fig 5; 7app; English.
XX
CC   The invention relates to mouse and human Ret ligand 5 (Ret15)
CC   polypeptides. The Ret15 polypeptides can be expressed by standard
CC   recombinant methodology. The Ret15 when bound to Ret, acts as a
CC   dimerization or autophosphorylation activator. The polypeptides and their
CC   antibodies are useful for stimulating growth of or limiting damage to,
CC   Ret expressing tissue in a subject, for suppressing growth of a tumour
CC   cell that expresses Ret, for modulating Ret signal transduction involving
CC   a cell expressing the Ret polypeptide. The Ret15 polypeptides, fusion
CC   proteins containing Ret15 and antibodies are useful for stimulating renal
CC   tissue growth and/or survival, supporting renal function and minimizing
CC   damage to renal tissue after various insults, particularly for treating
CC   acute renal failure, acute nephritis, chronic renal failure, nephrotic
CC   syndrome, renal tubule defects, kidney transplants, toxic injury, hypoxic
CC   injury and trauma. The compounds are also useful for treating conditions
CC   such as neural degeneration where neural growth and regeneration are
CC   desirable, e.g., Alzheimer's disease, Parkinson's disease, Huntington's
CC   disease, Tourette's syndrome, amyotrophic lateral sclerosis, as well as
CC   motor neuron disease, demyelinating disease, bacterial diseases, viral
CC   diseases, and prion diseases including Creutzfeldt-Jakob disease. The
CC   compounds are also useful for treating disorders due to neural
CC   tissue caused by neoplastic impingement, trauma or cerebrovascular events
CC   such as hemorrhage or emboli, and neural disorders such as mental
CC   retardation, autism, fetal alcohol syndrome, Down's syndrome and cerebral
CC   palsy. The present sequence represents the human Ret15 cDNA sequence
XX
SQ   Sequence 849 BP; 90 A; 330 C; 281 G; 148 T; 0 U; 0 Other;

Query Match   42.4%; Score 427.4; DB 4; Length 849;
Best Local Similarity 77.0%; Pred. No. 1.5e-81;
Matches 537; Conservative 0; Mismatches 151; Indels 9; Gaps 1;

Qy   124 GGGTCAGCGAGCTCCACTCAGAGGGAAATCGCTGCTGTCCGGAGCACGTGCACAGCA 183
         |||| |||||||||| |||| |||||||| ||| ||| ||||||||| | |
Db   46 GGGGTCCGGCGAGCTCGTCCGGAGGGAACCGATGTGTGGGACCGCGGAAGCCTGCACGGCG 105

Qy   184 GACGAGCAGTGCCAGCAGCTGCGCTCCGAGTACGTGGCGGCGCAATGCCCGGGCGGGGC 243
         ||| | || ||||||| |||| |||||||| |||||| | | |||||| ||| |
Db   106 GACGCGCGGTTGCCAGCGCGTTTGGCGCTCCGAGGTATGTGGGCGCCAGTGCCTGGGCGGGC--- 161

Qy   244 TGGGCGGGGACCCGGGAGAGCTGCGTGCGTGCGCTCCGGGCGTGCCCGTGGCGGCGCTTCTC 303
         |||||| | || |||||| |||||| |||| || |||||| | |||||||||| ||||||||
Db   162 ------TGGCGGAGCGGGGCGGCCGCTGTCCCGGCGGGCCCCGGCGCCGGCGCTTCTTC 216

Qy   304 GCGCCGCCGGGCGGGGCCCTTCCGGCGGCTCACCGCACGCGGCGTCTTCTGCGGATGCAAGGGCGCGCGGG 363
         || ||| ||||| | || |||||| |||||| |||||||||| |||||||||| | ||| |||||| | |
Db   217 GCCCCGCGGGGCCGCCTCCTGCCTTGAGCCCTTAAACTTCTCGGAGGCCAGCGGGGTCTGCGAGGGCCTT 276

Qy   364 TGCGCCGAGCCCGGCGGGCGGCCAGACATTCGCGCCCGCGGCTTCTCCGGGCCCCCAGCTG 423
         |||||||||| | ||||||| ||||| ||| || ||||| ||| |||| |||||||||||
Db   277 TGCGCCGAGCGGTCGGGCGCCCAGAGACCTTCGTGCGCCCGCTCGGGCTTTTCGGGGGCCCCC 336

Qy   424 GCGCCACCTTCCTCCTGCGAAGCGCCGGCGCCGGGGCCGCGCCCGGGGCCCC 483
         |||| ||| || || || |||||| |||||||||| | ||||||||||||
Db   337 GCGGCGCCCCTCCTCTTGAGCCCTTAAACTTCTCGGAGGCCAGCGGGGTCTGCGAGGGCCTT 396

Qy   484 CGTCTCTTTGCCTTCCAGGCCCTCCATTGCGCTCCCCGGCGGCTCCCGGCCGCACGGCGGCTGTTCCG 543
         || ||| || ||||||| | |||| | ||| | || ||||||| |||| | || |||||||||||
Db   397 CGCCTCCTTGGCCTTTCAGGTCTCGTGCACCCCAGCGCCCAGCGGGTCTGCCTG 456

Qy   544 GAGGAGGGGGGGCCCCCGGGGGTGTCTGGGCGCCTACGCGAGGGCCTTGTGTAGGCACCGGTGGTTCACC 603
         ||||| ||||| |||||| ||| || || |||||||||||||||||||||| |||||||||||||| |||
Db   457 CTGGACACAGGGGCGCCGCCGCTCCGGCGCCTACGCGAGGGCCTTGTGGTAGGCACCGGTGGTCACC 516

Qy   604 CCCAACTACCTGGACAAACGTGAGCGCCGCGGCCTTGCGCGTGTGAGGCCAGC 663
         || |||||| |||||||| ||||||||||| | |||||||| ||||||||||||
Db   517 CCTAACTACGTGGACAACGTGAGCGCGCGGGCCTTGCGCGGTGTGAGGCCAGC 576

Qy   364 TGCGCCGAGCCCGGCGGGCGGCCAGACATTCGCGCCCGCGGCTTCTCCGGGCCCCCAGCTG 423
Db   277 TGCGCCGAGCGGTCGGGCGCCCAGAGACCTTCGTGCGCCCGCTCGGGCTTTTCGGGGGCCCCC 336

Qy   424 GCGCCACCTTCCTCCTGCGAAGCGCCGGCGCCGGGGCCGCGCCCGGGGCCCC 483
Db   337 GCGGCGCCCCTCCTCTTGAGCCCTTAAACTTCTCGGAGGCCAGCGGGGTCTGCGAGGGCCTT 396

Qy   484 CGTCTCTTTGCCTTCCAGGCCCTCCATTGCGCTCCCCGGCGGCTCCCGGCCGCACGGCGGCTGTTCCG 543
Db   397 CGCCTCCTTGGCCTTTCAGGTCTCGTGCACCCCAGCGCCCAGCGGGTCTGCCTG 456

Qy   544 GAGGAGGGGGGGCCCCCGGGGGTGTCTGGGCGCCTACGCGAGGGCCTTGTGTAGGCACCGGTGGTTCACC 603
Db   457 CTGGACACAGGGGCGCCGCCGCTCCGGCGCCTACGCGAGGGCCTTGTGGTAGGCACCGGTGGTCACC 516

Qy   604 CCCAACTACCTGGACAAACGTGAGCGCCGCGGCCTTGCGCGTGTGAGGCCAGC 663
Db   517 CCTAACTACGTGGACAACGTGAGCGCGCGGGCCTTGCGCGGTGTGAGGCCAGC 576

Qy   664 GGAAACCCGCGCGAAGAGTTGCGAGAGCCTTCCGAGCGCTTTTTACAAGGAACCCCTTGCTTG 723
Db   577 GGGAACCGGCGGTGAGGACTCCGACCGCTCTTTACCAGGAACCGCGTGCTTG 636

Qy   724 GATGGTGCCATACAAGCCTTTGACAGCTGCCAACCATCAGTTCTGCAGGACCAGTGGAAC 783
Db   637 GATGGTGCCATTCAGGCCTTTGCCAGCGGGCCCCCAGTCTTCCTGCTGGACCACAGCTGAAC 696

Qy   784 CCCTACCAGAATGCTGGGCAGGCCAAGGTGGAGG 817
Db   697 CCCCAGGGGAGACCCGGAGCACAGCCTCCTCGCAGG 730

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OM nucleic - nucleic search, using sw model

                GenCore version 5.1.6
                Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:         February 18, 2005, 01:07:53 ; Search time 3963 Seconds
                                             (without alignments)
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Title:          US-10-019-337B-7
Perfect score:  1008
Sequence:       1 ctggtaagcttaagcgcaga.........aactcccctgccctcaggtc 1008
Scoring table:  IDENTITY NUC
                Gapop 10.0 , Gapext 1.0
Searched:       34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters:  68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      1: gb_est1:*
                2: gb_est2:*
                3: gb_htc:*
                4: gb_est3:*
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                6: gb_est5:*
                7: gb_est6:*
                8: gb_gss1:*
                9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                               SUMMARIES

                     %         Query
Result                 Match    Length  DB  ID              Description
No.     Score
------  -----         -----    ------  --  --              -----------
  1     395.2         39.2      950    5   BU514417         BU514417 AGENCOURT
  2     391.4         38.2      796    5   BU847383         BU847383 AGENCOURT
  3     387.6         38.5      679    6   BY733470         BY733470 BY733470
  4     385.6         38.3      805    5   BU559540         BU559540 AGENCOURT
  5     382.6         38.0     1084    3   AK090192         AK090192 Mus muscu
  6     378.4         37.5      704    7   CK835860         CK835860 4060515 B
  7     258.8         25.7      792    1   AU035938         AU035938 AU035938
  8     235.2         23.3      955    5   BU604828         BU604828 AGENCOURT
  9     217           21.5      499    5   BX516124         BX516124 BX516124
 10     206           20.4      454    2   BF565913         BF565913 UI-R-BO1-
 11     202           20.0      497    5   AA823200         AA823200 vw41h08.r
 12     170           16.9      788    7   CO884025         CO884025 BovGen_12
 13     148           14.7      735    5   BX101753         BX101753 BX101753
 14     143.8         14.3      633    6   CB097266         CB097266 554198 MA
 15     139.6         13.8      822    7   CN539269         CN539269 UI-M-HU0-
 16     135.8         13.5      699    4   BM724059         BM724059 UI-E-EO1-
 17     132.2         13.1      581    4   BI539556         BI539556 452275 MA
 18     132           13.1      537    2   AW632211         AW632211 91943 MAR
 19     131.6         13.1      806    7   CK028763         CK028763 AGENCOURT
 20     131           13.0      845    6   CA487292         CA487292 AGENCOURT
 21     130.4         12.9      538    4   BM363287         BM363287 BS320054B
 22     129.2         12.9      205    1   AI465648         AI465648 vw41h08.y
 23     129.2         12.8      205    1   AK076171         AK076171 Mus muscu
 24     128.8         12.8     4191    3   BC040251         BC040251 Mus muscu
 25'    125           12.4      395    6   CB776051         CB776051 AMGNNUC:S
 26     123.6         12.3      602    5   CA887225         CA887225 B0135E01-
 27     123           12.2      904    5   BU956631         BU956631 AGENCOURT
 28'    122.2         12.1      662    4   BI196287         BI196287 602755202
 29     121.2         12.0      419    8   A2715993         A2715993 RPCI-24-8
 30     120.8         11.8      942    5   BU857306         BU857306 AGENCOURT
 31     119           11.7      742    4   BI917824         BI917824 603183943
 32     117.8         11.7     4383    3   BC011532         BC011532 Mus muscu
 33     117.2         11.7     4618    3   BC044783         BC044783 Mus muscu
 34     112.8         11.2      446    1   AA518362         AA518362 v1i0d02.r
 35     111.4         11.2      631    5   AA387098         AA387098 vc18b07.r
 36     111           11.1      969    5   BU955785         BU955785 AGENCOURT
 37     110           10.9      823    7   CN232349         CN232349 WL8049A05
 38     106.4         10.6      772    6   CB526842         CB526842 UI-M-FY0-
 39     105.8         10.5      669    6   CD775377         CD775377 UI-M-AQ0-
 40     105.4         10.5      541    2   AW372400         AW372400 RC6-BT033
 41     104           10.3      541    2   AW372400         AW372400 RC6-BT033
 42     103.6         10.3      890    5   BX709568         BX709568 BX709568
 43      98.2         10.1      873    1   AL552892         AL552892 AL552892
 44      97            9.6      562    5   BX857143         BX857143 BX857143
 45      95.6          9.5      183    2   BE655865         BE655865 UI-M-BG0-
 45      95            9.4      183    2   BE655865         BE655865 UI-M-BG0-
```

                               ALIGNMENTS

```
RESULT 1
BU514417
LOCUS           BU514417                 950 bp    mRNA    linear   EST 12-SEP-2002
DEFINITION      BU514417 AGENCOURT 10119656 NIH_MGC_134 Mus musculus cDNA clone
                IMAGE:6511038 5', mRNA sequence.
ACCESSION       BU514417
VERSION         BU514417.1  GI:22821943
KEYWORDS        EST.
SOURCE          Mus musculus (house mouse)
  ORGANISM      Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE       1  (bases 1 to 950)
  AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
  TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL       Unpublished (1999)
COMMENT         Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Dr. David Rowe
                cDNA Library Preparation: Invitrogen Corp
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Agencourt Bioscience Corporation
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLAM14080 row: o column: 07
                High quality sequence stop: 573.
FEATURES             Location/Qualifiers
     source          1..950
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6511038"
                     /clone_lib="NIH_MGC_134"
                     /tissue_type="undifferentiated limb"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
                     this is a NIH_MGC Library."
ORIGIN

Query Match             39.2%;  Score 395.2;  DB 5;  Length 950;
Best Local Similarity   82.4%;  Pred. No. 3.8e-81;
Matches  496;  Conservative  0;  Mismatches  88;  Indels  18;  Gaps  3;

Qy        415 CCCCAGCTGGCGCGCCACCTTCCTGCCTGAAGCCCTTGGACCCCGCTGCGGAGCGCCGCGG 474
```

RESULT 2

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LOCUS       BU847383               796 bp    mRNA    linear    EST 16-OCT-2002
DEFINITION  AGENCOURT_10351125 NIH_MGC_144 Mus musculus cDNA clone
            IMAGE:6591416 5', mRNA sequence.
ACCESSION   BU847383
VERSION     BU847383.1  GI:24032092
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 796)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
            cDNA Library Preparation: Michael Brownstein Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2812 row: p column: 08
            High quality sequence stop: 399.
FEATURES             Location/Qualifiers
     source          1..796
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6591416"
                     /lab_host="DH10B (T1-phage-resistant)"
                     /clone_lib="NIH_MGC_144"
                     /note="Organ: Brain; Vector: pDNR-LIB; Site 1: SfiI
                     (ggccattatggcc); Site 2: SfiI (ggccgctcggcc); cDNA made
                     by oligo-dT priming and directionally cloned. 5' and 3'
                     adaptors were used in cloning as follows:
                     5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length
                     enriched library was constructed using the Clontech
                     Creator SMART kit and size-selected to contain the 0.2-0.5
                     kb size fraction (other fractions present in NIH_MGC_143).
                     Library created in the laboratory of M. Brownstein (NIMH,
                     NIH). Note: this is a NIH_MGC Library."
ORIGIN
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Qy Query Match    38.8%;  Score 391.4; DB 5;  Length 796;
Best Local Similarity  83.1%;
Matches  488;  Conservative   0;  Mismatches  81;  Indels  18;  Gaps  3;
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Qy    430 CCTTCCCTGCCTGAGGCCCTTGGACCACCATCAGTTCTCGCAACCATCAGTTCTCGCAGGA 489
          ||| || |||||| |||||||||||||||||||||||  |||||||||||||||||||||||
Db      5 CGTGCGGTGCGGGGCGGGGGCGGGGGGCTGGTGGTGGCCGCCGGGGCCGGGGCCCGGTCTC  64
```

```
Qy    490 TTTGCCTTCCAGGGGCTCATGCGCGGGGGGGCCCTCCCGGGGGGGGCGGGGGCGTCCGGAG 549
          |||||| |||||||||||||||| |||||||||||||||||||||| |||||||||||||||
Db     65 CTTGCCTTCCAGGGCTCCATGCGCTCCGGGGGGGGCCCTCCGGGGCCGGGGCCCTGCAGGAG 124
```

```
Qy    550 GGGGGGCGCCCGGGGTGTCTGCGCGCCTACGCACGGCCGCCCTTGTAGGCACCCCCCCAAC 609
          |||||| |||||| || ||||||||| ||||||||||||||||||||||||||||||||||
Db    125 GGGGGGCCCCGGGGTTGTCTTGCGCGTCAGGCCGCCCTCATAGGCACCGGTCACCCCCCAAC 184
```

```
Qy    610 TACCTGGACAACGTGAGCGGCGGCGGCGGCGGCGGGGCCCCTTCGCAAGGCTTTTTACAAGG 669
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185 TACCTGGACAACGTGAGCGCCGCCGGCGGTGGTCACCCCCAAC 244
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```
Qy    670 CGGCGCGGAACGATGCGGAAGCCTTCGCAAGCTTTTACAAGGAACCCCTGCTTGGAACCCTAC 729
          |||| |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    245 CGGGGCGGAAGAATGCGGAAGCCTTCCCGAAGCGTTCGGCGGCGTCGTGGCCCAGTGGGAAC 304
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Qy    730 GCCCATACAAGCCTTTGACAGCTCCAAGGTGGAGGCCGGGGGCCGGGGCCAGTGGGAACCCCTAC 789
          ||||||||||||| ||||||||||| |||||||||||||||||||
Db    305 GCCCATACAAGCCTTTGACAGCCTTCTGCAGCCATCAGTTCTCGCAGGAG---------AC 354
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RESULT 3

```
LOCUS       BY733470               679 bp    mRNA    linear    EST 17-DEC-2002
DEFINITION  BY733470 RIKEN full-length enriched, 16 days neonate male
            diencephalon Mus musculus cDNA clone G63001SH18 5', mRNA sequence.
ACCESSION   BY733470
VERSION     BY733470.1  GI:27146597
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
```

```
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1  (bases 1 to 679)
AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
          Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
          Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
          Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
          Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
          Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
          Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
          Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
          Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
          Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
          Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
          Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
          Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
          Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
          Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
          Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
          Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
          Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
          Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
          Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
          Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
          Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
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          Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
          Itoh,M., Kagawa,I., Miyazaki,A., Sasaki,K., Sasaki,K., Shibata,K.,
          Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
          Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE     Analysis of the mouse transcriptome based on functional annotation
          of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
PUBMED    12466851
MEDLINE   22354683
COMMENT   Contact: Yoshihide Hayashizaki
          Laboratory for Genome Exploration Research Group, RIKEN Genomic
          Sciences Center(GSC), Yokohama Institute
          The Institute of Physical and Chemical Research (RIKEN)
          1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
          Tel: 81-45-503-9222
          Fax: 81-45-503-9216
          Email: genome-rep@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
          Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
          Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
          Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
          Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
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          Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
          Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
          Direct Submission
          Computational Analysis of Full-Length Mouse cDNAs Compared with
          Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
          Normalization and subtraction of cap-trapper-selected cDNAs to
          prepare full-length cDNA libraries for rapid discovery of new
          genes. Genome Res. 10 (10), 1617-1630 (2000)
          RIKEN integrated sequence analysis (RISA) system--384-format
          sequencing pipeline with 384 multicapillary sequencer. Genome Res.
          10 (11), 1757-1771 (2000)
          Computer-based methods for the mouse full-length cDNA
          encyclopedia: real-time sequence clustering for construction of a
          nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
          cDNA library was prepared and sequenced in Mouse Genome
          Encyclopedia Project of Genome Exploration Research Group in Riken
          Genomic Sciences Center and Genome Science Laboratory in Riken.
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues.
          Please visit our web site (http://genome.gsc.riken.go.jp) for
          further details.
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Matches  489;  Conservative   0;  Mismatches  89;  Indels  18;  Gaps   3;

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BU559540
BU559540
LOCUS       BU559540                805 bp     mRNA    linear    EST 16-SEP-2002
DEFINITION  AGENCOURT 10336959 NIH_MGC_144 Mus musculus cDNA clone
            IMAGE:6588321 5', mRNA sequence.
ACCESSION   BU559540
VERSION     BU559540.1  GI:22909836
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 805)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

RESULT 5

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2804　row: o　column: 09
High quality sequence stop: 527.

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　　　　　　　　by oligo-dT priming and directionally cloned. 5' and 3'
　　　　　　　　adaptors were used in cloning as follows:
　　　　　　　　5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
　　　　　　　　5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length
　　　　　　　　enriched library was constructed using the Clontech
　　　　　　　　Creator SMART kit and size-selected to contain the 0.2-0.5
　　　　　　　　kb size fraction (other fractions present in NIH_MGC 143).
　　　　　　　　library created in the laboratory of M. Brownstein (NIMH,
　　　　　　　　NIH). Note: this is a NIH_MGC Library."

ORIGIN
　Query Match　38.3%;　Score 385.6;　DB 5;　Length 805;
　Best Local Similarity　86.6%;　Pred. No. 6.4e-79;
　Matches 466;　Conservative 0;　Mismatches 54;　Indels 18;　Gaps 3;

Qy　479 GGGCCCCGGTCTCTTGCCTTCCAGGCTCCCATGCGCCTCCCCGCGCCTCCCCGGACGGCT 538
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Qy　539 GTCCGGAGAGGGGGGGGGGGGTTCTGGGCGCCCTACGGCGAGGCCCTTGTAGGCACCGTGG 598
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Db　241 GCTTCGGATGGTGTGCCCATACAAGCCTTTGACAGCTTCGCCATCCAGTTCTCTGCAGGACCAG- 299

Qy　779 GGAACCCCTACCCAGAATGCTGGGGCAGGGCCAAGGTGGAGGCCTGAGTGGCCTGAGAGAGA 838
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DEFINITION　　　Mus musculus 16 days neonate male diencephalon cDNA, RIKEN
　　　　　　　　full-length enriched library, clone:G630015H18 product:glial cell
　　　　　　　　line derived neurotrophic factor family receptor alpha 4, full
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ACCESSION　　　AK090192
VERSION　　　　AK090192.1　GI:26355273
KEYWORDS　　　HTC; CAP trapper.
SOURCE　　　　Mus musculus (house mouse)
　ORGANISM　　Mus musculus
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　　　　　　　Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE　　　1
　AUTHORS　　　Carninci,P. and Hayashizaki,Y.
　TITLE　　　　High-efficiency full-length cDNA cloning
　JOURNAL　　　Meth. Enzymol. 303, 19-44 (1999)
　MEDLINE　　　99279253
　PUBMED　　　10349636
REFERENCE　　　2
　AUTHORS　　　Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
　　　　　　　Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
　TITLE　　　　Normalization and subtraction of cap-trapper-selected cDNAs to
　　　　　　　prepare full-length cDNA libraries for rapid discovery of new genes
　JOURNAL　　　Genome Res. 10 (10), 1617-1630 (2000)
　MEDLINE　　　20499374
　PUBMED　　　11042159
REFERENCE　　　3
　AUTHORS　　　Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
　　　　　　　Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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　　　　　　　Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
　　　　　　　Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
　TITLE　　　　RIKEN integrated sequence analysis (RISA) system-384-format
　　　　　　　sequencing pipeline with 384 multicapillary sequencer
　JOURNAL　　　Genome Res. 10 (11), 1757-1771 (2000)
　MEDLINE　　　20530913
　PUBMED　　　11076861
REFERENCE　　　4
　AUTHORS　　　The RIKEN Genome Exploration Research Group Phase II Team and the
　　　　　　　FANTOM Consortium.
　TITLE　　　　Functional annotation of a full-length mouse cDNA collection
　JOURNAL　　　Nature 409, 685-690 (2001)
REFERENCE　　　5
　AUTHORS　　　The FANTOM Consortium and the RIKEN Genome Exploration Research
　　　　　　　Group Phase I & II Team.
　TITLE　　　　Analysis of the mouse transcriptome based on functional annotation
　　　　　　　of 60,770 full-length cDNAs
　JOURNAL　　　Nature 420, 563-573 (2002)
REFERENCE　　　6　(bases 1 to 1084)
　AUTHORS　　　Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
　　　　　　　Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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　　　　　　　Muramatsu,M. and Hayashizaki,Y.
　TITLE　　　　Direct Submission
　JOURNAL　　　Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
　　　　　　　Physical and Chemical Research (RIKEN), Laboratory for Genome
　　　　　　　Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
　　　　　　　RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
　　　　　　　Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
　　　　　　　URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
　　　　　　　Fax:81-45-503-9216)
COMMENT　　　cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES   Location/Qualifiers
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ORIGIN

Query Match   38.0%; Score 382.6; DB 3; Length 1084;
Best Local Similarity   82.1%; Pred. No. 3.3e-78;
Matches 495; Conservative   0; Mismatches 89; Indels 19; Gaps 4;

Qy   415 CCCCAGCTGGCGCCACCTTCCTGCCCTGAAGCCCTTGGACCCCTGCGAGCGAAGCCCCCCG 474
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Qy   475 TGCCCGGCCCCGCTCTCTTTGCCTTCCAGGCCTTCATGGCCTCTCCGGCGTTCCCGGGGAC 534
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DEFINITION 4060515 BARC 8BOV Bos taurus cDNA clone 8BOV_14I17 5', mRNA
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ACCESSION   CK835860
VERSION   CK835860.1   GI:45067634
KEYWORDS   EST.
SOURCE   Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1 (bases 1 to 704)
AUTHORS   Baumann,R.G.; Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
            Matukumalli,L.K.
TITLE   Construction and Analysis of a cDNA Library Generated From
            Intestinal Muscle and Epithelial Tissues of Holstein Cattle
JOURNAL   Unpublished (2004)
COMMENT   Contact: Richard G. Baumann
            Bovine Functional Genomics Lab
            ANRI
            BLDG 162; BARC-EAST, Beltsville, MD 20705, USA
            Tel: 3015048744
            Fax: 3015048744
            Email: rbaumann@anri.barc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            0.000925 using options -trim alt '' -trim fasta. Vector identified
            by cross match using options -minmatch 12 -minscore 12
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                  /dev_stage="Lactating, Neonatal"
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                  NotI; Site 2: EcoRI; Normalized cow cDNA intestinal
                  library in pCMVsport6.1, constructed from equimolar mRNA
                  pools derived from 5 sources, 4 lactating intestinal, 1
                  neonatal intestinal 4/5 Lactating, Proximal Duodenum,
                  Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
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ORIGIN

Query Match   37.5%; Score 378.4; DB 7; Length 704;
Best Local Similarity   74.8%; Pred. No. 3e-77;
Matches 491; Conservative   0; Mismatches 156; Indels 9; Gaps 1;

Qy   887 ATACTCACTGACCTGCCTCTCCAGGCCTCGGTTCTCTGGGATTA-TGCTCACTGAACTGAAACTCCCTTGCCCTCAG 946
           |||| |||||||||||| | |||||||| | ||||||| ||||| ||| ||||| |||||| ||||||| |||||
Db   480 GCACTCACTGCCCTGCCTCTCCAGGCCTCTGGCTCTGCTTCTGATTAGGAACATGAACCCGTGGACGGCAC 539

Qy   947 ACAGCTGACTGCCCATGTCTCTGGGATTA-TGCTCACTGAACTCCCTTGCCCTCAG 1005
           ||||||| |||| |||||| || |||||| ||| |||| |||| |||||||||||
Db   540 ACAGCTGACTGCCCATGTCTCCGGATGACTGCTCACTGACTGAAAACTCCCTTGCCCTCAG 599

Qy   1006 GTC 1008
           |||
Db   600 GTC 602

Qy   164 CAGCCCGAGGCCTGCACAGCAGACGACGACGACGTCCACGAGCGTCGCGAGCCGGTGGCGC 223
           ||||| |||||| || ||| |||| || || || |||| ||| | || ||| || |||
Db   1 CGGCCCGAGCGGTGCACGCGCACCGCGCGAGGCGTGCCATCGGCCGTGCCATCGGCGGTGGCGC 60

RESULT 7

LOCUS   AU035938   792 bp   mRNA   linear   EST 12-JUL-2000
DEFINITION   AU035938 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-1073,
               mRNA sequence.
ACCESSION   AU035938
VERSION   AU035938.1 GI:3718946
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 792)
  AUTHORS   Sasaki,Z., Suzuki,Y., Watanabe,M., Imai,J., Shibui,A., Yoshida,K.,
               Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S.
  TITLE   Construction of mouse full length-enriched cDNA libraries
  JOURNAL   Unpublished (1998)
  COMMENT   Contact: Katsuyuki Hashimoto
               Division of Genetic Resources
               National Institute of Infectious Diseases
               23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
               Email: khashi@nih.go.jp
FEATURES   Location/Qualifiers
     source   1..792
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="MNCb-1073"
                     /sex="female"

Qy   224 AATGCCCTGGGCGCCGGGCGGGGGGCTGGCGCGGGAGAGGCTGGGCGGGCGCTCCGGTGCGGCC 283
Db   61 AGTGCGCTTGGGTCGTGCC------------CGCGCGGGGAGGGCTGGCCCCCGCGGCCGGCTGCGGCC 111

Qy   284 GTGGCCCTGGGCGCCCGGCGTTCTTCTTCGCCCTGGCCACGCGGGCTGCTTCTTCT 343
Db   112 GCGCCCTGCGCCACTTCTTCGCCCC------CGGGGGGGGGGGGCTTACCCACGCCACTGCTTCTTCT 171

Qy   344 GCCGGATGCGAAGGCCCGGGCGTGCGCGCGACGGGGGCCCCGCCCCCGGGGGGGCCTGCG 403
Db   172 GCCCTTGCGGCGGCGGGGCGGGGTGCGGCGAGAGGCGGCCAGGAACCTTCGTGCCCTTCCTGCGG 231

Qy   404 CGTTCTCCGGCGGCCCCCGAGCGTGGCGCCCCGGGGAGCCCTTGGACCGGCTTGCGAGC 463
Db   232 CTTTCTCAGGGCCCTGGGCCGGGGGCCACCTTCCTCGGGGCCTTAGAATGCGTTGCGAGC 291

Qy   464 GAAGCGCGGCGGTGCGGGCCCGTTCTTTGCCTTCCAGGGCCTCATGCGGTCCCGGGCCCG 523
Db   292 ACAGCCGGATCTGCAGGGCCCCGCCCCTGGCCTTCCAGGTTCTCCCTGTGCGGGTGCGGGGCCCG 351

Qy   524 GCTCCCGCCACGCGCTGTCCGGAGGAGGGGGGCCCCGGGTTGTCTGCGGGTTCTCCGGCCCCCAGCT 583
Db   352 GCAACCCTACACGGTGCTCCGAGACCAAGCCCCCAGCTGCGCCCCCGGGTTCTCCGGGGGTT 411

Qy   584 TTCGTAGGCACCGTGGTGTCACCCCCAACTACTACTGACAAACGTGAGAGGGCCGGTTCGGCCCCT 643
Db   412 TCGTGGGCGCACAGCCATCACCGCCCCCAACTACGTGAGGCAGAACCCCTGGAGGCGCACCCGGTGTGCCGGCCCT 471

Qy   644 GGTGCGGCTTGTGAGGCGGGCAGGGAACGGGCGGGAAGAGTCGAAGCCTTTCGGCAAGCTTT 703
Db   472 GGTGCGGACTGCAGAGCGGCCACGCGGAAATCGGCGTGGAGGAGTGGGAGGAGTCTTCCGGGAGGCGTCT 531

Qy   704 TTACAAGGAACCCCTGCCTTGGATGGTGCCATACAAGCCTTTGACAGCTCGCAACCATCAG 763
Db   532 TTACGAGGAGAACCGGCTGCTTGGACAGTGCCATACAGAACCTTTGACGGGGAGGCCCCCCAA 591

Qy   764 TTCTTCTGCAGGACCACGTGGAACCCCTACCACGAAATGCTGTGGGGCCGGAGGCCAAGGTGGGAGGCC 819
Db   592 TCCTTACGTAACCAACTGGACTCCCACCAGAGACCCCTGAGCGAGAGTCTCCTGCAGGTC 647

ORIGIN

Query Match   25.7%; Score 258.8; DB 1; Length 792;
Best Local Similarity 80.9%; Pred. No. 1.9e-49;
Matches 338; Conservative 0; Mismatches 27; Indels 53; Gaps 1;

Qy   363 GTGCGCGGAGCGCCGGCGCCAGACATTCCGCGCGCCCGGGCCGGTTCTCCGGCCCCCAGCT 422
             |||||||||| | | | |||||||||||||| |||||||||||||||||||||||||
Db   1 GTGCGCGGAGCGCCGGCGCCAGACTTTCCGCGCGCCCCCGGGCCGGTTCTCCGGGGGGTT 60

Qy   423 GGCGCCCACTTCTCCTGGCCCGAAAGCCCCTTGACACCGTGCGAGGAAGCGCGCGGGTGCC----- 478
             |||| |||||||||| |||||||| |||||||||||||||||||||||||||||
Db   61 GGTGCGCGCCCTCTTCGCCCTGGAGGCCCTGAGGCGGTGCGGACCGCGCACCCGGTGTGCCGGGTG 120

Qy   479 -----------------------------------GGCCCCGTCTC 489
                                                ||||||||||
Db   121 CGTGCCGGGGGCGGGGCTGGGGGGCTGCCACCGGTCCCGGCCCCCGGTCTC 180

Qy   490 TTTGCCTTCCAGGGCCTCATCGCCCGGCGCCCCGGGCGACGGGCTCTCCGGGGAGGAG 549
             |||||||||||||||| |||| ||||||||||||||||||| |||||||||||||
Db   181 CTTGCCTTCCAGGGCCCTCATCGCGCTCCCCGGGCGGGGCCGCGGGGGAGGAG 240

Qy   550 GGGGGCCCCCGGCCGCGTGTCCTGCGGCCCTTAGGCAGCCCTTGTTGGTGGTTCACCCCCCAC 609
             |||||||| |||| ||||||||||||||||||||||||||||||| |||||||||
Db   241 GGGGGCCCCCGGCCGGTTGTCTGCGCCGTCACCGAGGCCCTCATGGCCACCCCAC 300

Qy   610 TACCTGGACAACGTGAGCGGCGGCGGCGGGGCGTTGCGCCCGGCGTTGTGAGGCGGGAAAC 669
             ||||||||||||||||||||||||||||||||| |||| |||| | |||||||| |||
Db   301 TACCTTGGACAACGTGAGCGGGGGGCGGGGCGTTGCCCCCGGCGGGGGCGGGGAAAC 360

Qy   670 CGGCCCGGAACGAAATGCGAAAGCCTTCGCAAGCTCTTTACCAAGGCAACCCCTGCTTGGATG 727
             |||||||||||| ||||||||||| ||||| ||||||||||||| |||||||||||||
Db   361 CGGCCCGGAACGAAATGCGAAAGCCTTCGCAAGCTCTTTACCAAGGCAACCCCTGCTTGGGGTG 418

RESULT 8

LOCUS   BU604828   955 bp   mRNA   linear   EST 20-SEP-2002
DEFINITION   AGENCOURT 10055539 NIH_MGC_144 Mus musculus cDNA clone
               IMAGE:6535992 5', mRNA sequence.
ACCESSION   BU604828
VERSION   BU604828.1 GI:22356587
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 955)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: Dr. Michael Brownstein
               cDNA Library Preparation: Dr. Michael Brownstein Laboratory
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be

COMMENT   found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLCM2696 row: j column: 24
               High quality sequence stop: 203.
FEATURES   Location/Qualifiers
     source   1..955
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6535992"
                     /clone_lib="NIH_MGC_144"
                     /lab_host="DH10B (T1-phage-resistant)"
                     /note="Organ: Brain; Vector: pDNR-LIB; Site_1: SfiI
                     (ggccgcccggcc); Site_2: SfiI (ggccattatggcc); cDNA made
                     by oligo-dT priming and directionally cloned; 5' and 3'
                     adaptors were used in cloning as follows:
                     5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3', and
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3', Full-length
                     enriched library was constructed using the Clontech
                     Creator SMART kit and size-selected to contain the 0.2-0.5
                     kb size fraction (other fractions present in NIH MGC 143).
                     Library created in the laboratory of M. Brownstein (NIMH,
                     NIH). Note: this is a NIH_MGC Library."
ORIGIN

Query Match   23.3%;   Score 235.2; DB 5; Length 955;
Best Local Similarity   86.7%;   Pred. No. 5.8e-44;
Matches 274; Conservative   0; Mismatches   33; Indels   9; Gaps   1;

Qy   174 GTGCACAGCACGAGCGAGCAGTCGCAGCAGCTCCGAGTACGTGGCGCAATGCCTGGG 233
           ||||| ||| || ||||||||||| |||||| || |||||||||||||||||| ||||
Db   2 GGGTACAGCAGACGAGCGGGTGCCAGCAGCTCGCGTCTCGAGTACGTGGCACCGATGCCTGGG 61

Qy   234 CCGGGC---------GGGCTGGCGGGGGGACCCGGGGACTGCTGGCGCCTTCCCGCTCCGCCG 284
           ||||| |||||||||||||||||||||||||||||| || |||| |||||||||
Db   62 CCGGGCAGGCGCCCGGGCGGACCCGGGGACTGCTGGCGTGCGTCGGCTCCCGGTCGTGCCAGCG 121

Qy   285 TGCCCTGCGCGCCGCCTTTTCGCGCCGCCTTCGCGGCGGCTCACGCACGGCGTGCTCCTTTCTG 344
           |||||||||| ||||||||||| | ||||| |||||| || ||||| || || || |||| |||
Db   122 AGCCCTGGCGGCCGCCTTCTCGCGGTGGGCGTCCGGCTCCGGGCTTCTCGGCTGCTCTCTTCTG 181

Qy   345 CGGATCGGAAGGCCCCGCGGTCGCGCCCAGACATTCGGCGCCGGCCTTCGGC 404
           || ||| ||||||||||||| | ||| ||||||| ||||||||||| ||| ||
Db   182 CGGCTCGGAACGCTCCGCGCGTGCGCGGGCCCAGACTTTCGGCGGCGGGCCCTTGCGC 241

Qy   405 GTTCTCTCCGGCGCCCCAGCGTGGCGCGCCCACTTCCTCTGCTCCTGAAGCCCCTTGGACCCCCTTGCCGGAGCG 464
           |||||||||||||||||||||||||||||| | ||| ||||||||||||||||||||||||||||||||||||||||
Db   242 GTTCTCTCCGGCGCCCCAGGGTGGGTCGCGGGCGGTTGGGTCGGCGCCCTCTTTGCCTGGAGCGGGCGTCGCGAGCG 301

Qy   465 AAGCCCGCCGGGTGCCGG 480
           ||||| |||||||||||||
Db   302 CAGCCGCGCCCGTGTCCGG 317

RESULT 9
LOCUS   BX516124   499 bp   mRNA   linear   EST 27-JUN-2003
DEFINITION   BX516124 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
               IMAGP998D163136 ; IMAGE:1246431, mRNA sequence.
ACCESSION   BX516124
VERSION   BX516124.1   GI:32298747
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 499)
  AUTHORS   Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D.
               and Korn,B.
  TITLE   Mouse UnigeneSet - RZPD2
  JOURNAL   Unpublished (2003)
COMMENT   Contact: Ina Rolfs
               RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGP998D163136.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)
http://www.rzpd.de/ (RZPDLIB No.981)
bin/showlib.pl.cgi/response?libNo=981 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

               This clone is available royalty-free from RZPD;
               contact RZPD (clone@rzpd.de) for further information. Seq primer:
               T7, Primer sequence: TAATACGACTCACTATAGGG.

FEATURES   Location/Qualifiers
     source   1..499
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGp998D163136 ; IMAGE:1246431"
                     /strain="C57BL/6J"
                     /clone_lib="Soares_mammary_gland_NbMMG"
                     /note="Organ: mammary gland; Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGGCGGCGCGCGGAAATGGTTTTTTTTTTTTTTTTTTT
                     T 3'], double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                     constructed and normalized by Bento Soares and M.Fatima
                     Bonaldo."
ORIGIN

Query Match   21.5%;   Score 217;   DB 5; Length 499;
Best Local Similarity   82.3%;   Pred. No. 9.2e-40;
Matches 292; Conservative   0; Mismatches   45; Indels   18; Gaps   3;

Qy   662 GCGGAAAACCGGCGCGGAGAGTGCGAAGAGCCTTCCGCAAGCTTTTTACAAGGAACCCCTGCT 721
           || || || |||||||| || |||| ||| || || |||||||||| |||||||| ||||||||
Db   2 GTGGAAAACCGGCGCGGGAAGAAATGCGAAGACCCTTCCGGAAGCTCTTTTACAAGGAACCCCTGCT 61

Qy   722 TGGATGGTGCCATACAAGCCCTTTGACAGCTCGCCAACCATCAGTTCTCCCAGAGACCAGTCGA 781
           ||||||||||| |||| || |||||||||||| |||| ||||| ||||| |||||||| || |||
Db   62 TGGATGGTGCCATACAAGCCCTTTGACAGCTTGCCAGCCATCAGTTCTCCCAGAGACCAG---- 117

Qy   782 ACCCCTACCAGAAATGCTGGGCAGGCCAAGGTGGAGGGCCTGAGTGGGCCTGAGAAGAGCTGG 841
           | | || || |||||||||| | |||| |||| ||| ||| | ||||||||||||||
Db   118 A------ACTGCTGGGTGCTGTTCTCCCGCGGCCAAGGTGGACGAGTGGGCCTGAGAAGAGCTGG 171

Qy   842 AGGCAGAAAACGGTCCCCGTTTTTGT-------CCCAAGGTGTCCTCGATGTCCATACTCAC 894
           |||||||||||| ||| | |||||| |||||||||||||||| ||||||| |||
Db   172 AGGCAGAAACAGTCCTTGTTTTTGTCCTTAACGGCCCAAGGTGTCCTGGCGTGTCGCCACTCAC 231

Qy   895 TGCCCTGGCTCTCCAGGCCCCTGCTCTATAATTAGGAGAAGGTGAACCATCGACAACACAGCTGA 954
           |||||||||| |||||||||||||||| || |||||||| |||||||||||||||||||||||||
Db   232 TGCCCTGGCTCTCCAGGCCCCTGCTCTCGATTAGGACGGACCGGTGACGACACACAGCTGA 291

Qy   955 CTGCCCATGTCTCTGGATTA-TGCTCACTGAGACTGAAACTCCCTTGCCCTCAGGTC 1008
           ||||||| ||| ||| | || || ||||| | || ||||||||| ||||||||||
Db   292 CTGCCCATGTCTCCGATGACTGCTCACTGAGCTGAAACTCCCTTGCCCTCAGGTC 346

RESULT 10
LOCUS   BF565913
DEFINITION   UI-R-BO1-ajr-c-09-0-UI.r1 UI-R-BO1 Rattus norvegicus cDNA clone
               UI-R-BO1-ajr-c-09-0-UI 5', mRNA sequence.

Left record

```
ACCESSION   BF565913
VERSION     BF565913.1  GI:11675643
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 454)
AUTHORS     Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE       Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
MEDLINE     97044477
PUBMED      8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL. (info@image.llnl.gov). IMAGE ID=1798704
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1..454
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-BO1-ajr-c-09-0-UI"
                     /dev_stage="adult"
                     /lab_host="DH10B (life Technologies)"
                     /clone_lib="UI-R-BO1"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The library
                     (UI-R-BO1) is a subtracted library derived from a mixture
                     of the following tissues: thalamus, cerebellum,
                     hypothalamus, medulla, pons, midbrain, cerebral cortex,
                     corpus striatum and hippocampus. For a detailed
                     description of the library from which this clone was
                     derived, please visit our web site at
                     ratest.eng.uiowa.edu. The subtraction has been previously
                     described in (Bonaldo, Lennon and Soares, Genome Research
                     6:791-806, 1996)"
ORIGIN
```

```
Query Match    20.4%;  Score 206;  DB 2;  Length 454;
Best Local Similarity   100.0%;  Pred. No. 3.3e-37;
Matches 206;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    803 AGGGCCAAGGTGGGAGGGCCTGAGGAGAGAGGATGGGAGGAGGAGAGGTCCCCGTTT 862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5 AGGGCCAAGGTGGGAGGGCCTGAGGAGAGAGGATGGGAGGAGGAGAGGTCCCCGTTT 64
Qy    863 TGTGTCCCAAGGTGTCTCCGATGTCCATACTCACTCACTCCCCTGGCCTCCCCTGCTTCTCTAA 922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 TGTGTCCCAAGGTGTCTCCGATGTCCATACTCACTCACTCCCCTGGCCTCCCCTGCTTCTCTAA 124
Qy    923 TTAGGAAGGTGAACCATGGACAACACAGCTGACTGACTGCCCATGTCTCTGGATTATGCTCACTG 982
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 TTAGGAAGGTGAACCATGGACAACACAGCTGACTGACTGCCCATGTCTCTGGATTATGCTCACTG 184
Qy    983 AACTGAAAACTCCCCTTGCCCTCAGGGTC 1008
          |||||||||||||||||||||||||||||
Db    185 AACTGAAAACTCCCCTTGCCCTCAGGGTC 210
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Right record

```
LOCUS       AA823200      497 bp    mRNA    linear   EST 17-FEB-1998
DEFINITION  vw41h08.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
            IMAGE:1246431 5', mRNA sequence.
ACCESSION   AA823200
VERSION     AA823200.1  GI:2893068
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 497)
AUTHORS     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE       The WashU-HHMI Mouse EST Project
JOURNAL     Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            Washington University School of Medicine
            WashU-HHMI Mouse EST Project
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:660119
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 443.
FEATURES             Location/Qualifiers
     source          1..497
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1246431"
                     /sex="male"
                     /tissue_type="mammary gland"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares_mammary_gland_NbMMG"
                     /note="Organ: mammary gland; Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGACGGGCCGGCGAATGGTTTTTTTTTTTTTTTTTTTTTTTT
                     T 3'], double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                     constructed and normalized by Bento Soares and M.Fatima
                     Bonaldo."
ORIGIN
```

```
Query Match    20.0%;  Score 202;  DB 1;  Length 497;
Best Local Similarity   81.8%;  Pred. No. 2.8e-36;
Matches 288;  Conservative 0;  Mismatches 45;  Indels 19;  Gaps 4;

Qy    665 GAAACCGGCGGCGAGAGTGGGAAGGCCTTCGCAAGCTTTTACAAGGAACCCTGCTTGG 724
          |||| |||| |  | | ||  | || |||| ||||||| || ||||||||||||||||
Db      3 GGAACCGGCGCGGAAGGAAATGGGAA-CCTTCCGCAAGCTTCTTTACAAGGAACCCTGCTTGG 61
Qy    725 ATGGTGCCCATACAAGCCTTTGACAGCTTCGCCAACCATCAGTTCTTCCAGGACCAGTGGAACC 784
          |||||||||||||||||||||||||||||| |  | ||||||||||||| ||||||| |||||
Db     62 ATGGTGCCCATACAAGCCTTTGACAGCTTGACAGCCATCAGTTCTTGACAGCTTGCAG------ 114
Qy    785 CCTACCAGAATGCTTGGGACAGGCCCAAGGTGTGGAGGTGGAGCCTGAGGAGGAGGATGGGAGG 844
          |||||  | || |||||| |  ||  |||||||| ||| |||| |||||||||||||||||||||
Db    115 ---ACTGCTCGGGTGCTGTGTTTCCCGCGGGGCAAGGGCACGAGGTGGCCTGAGAGAGAGTGGAGG 171
Qy    845 CAGAAACGGGTCCCCGTTTTTGT------CCCAAGGTGTGTCCGATGTCCATACTCACTGC 897
          ||||| ||||||||||||| ||       |||| ||||| | |||| | | ||||   ||
Db    115 ------ACTGCTCGGGTGCTGTGTTTCCCGCGGGGCAAGGGCACGAGGTGGCCTGAGAGAGAGTGGAGG 171
```

RESULT 12
CO884025

```
LOCUS       CO884025              788 bp    mRNA    linear   EST 01-SEP-2004
DEFINITION  BovGen_12350 normal cattle brain Bos taurus cDNA clone
            RZPDp1056L20170 5', mRNA sequence.
ACCESSION   CO884025
VERSION     CO884025.1  GI:51813969
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 788)
  AUTHORS   Hennig,S., Janitz,M., Herwig,R. and Williams,J.
  TITLE     Generation, annotation, evolutionary analysis and database
            integration of 14969 cattle EST clusters
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Hennig S
            laboratory 123, dept. Lehrach
            Max-Planck-Institut fuer Molekulare Genetik
            Ihnestr.63-73, D-14195 Berlin, Germany
            Tel: +49 30 8413 1612
            Fax: +49 30 8413 1380
            Email: hennig@molgen.mpg.de
            The library was characterised by oligonucleotide fingerprinting
            (ONFP) to reduce sequencing redundancy. According to the ONFP
            procedure, clones that display the same hybridisation matrix with a
            battery of 200 8mer oligonucleotides are grouped into clusters. One
            clone per ONFP cluster was selected for sequencing. cDNA clones and
            filters are distributed via Deutsches Ressourcenzentrum fuer
            Genomforschung GmbH (http://www.rzpd.de).
            PCR Primers
            FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP) 5'-seq
            BACKWARD: 5' GCTATTACCCAGCTGGGCGAAAGGGGGATGTG 3' (M13FSP) 3'-seq
            Seq primer: 5'-CCGGTCGGGAATTCCCGGGT-3' (M13RSP).
FEATURES             Location/Qualifiers
     source          1..788
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="RZPDp1056L20170"
                     /sex="female"
                     /tissue_type="brain tissue"
                     /dev_stage="adult brain"
                     /clone_lib="normal cattle brain"
                     /note="Organ: brain; Vector: pSport1; Site_1: NotI;
                     Site_2: SalI; Random primed and directionally cloned in
                     pSport1 vector using NotI
                     (5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCC (T)15-3' and SalI 5'-
                     TCGACCCACGGTCCG-3' adapters (Gibco BRL)"
```

ORIGIN

```
Qy          172  CAGAAACAGTCCTTGTTTGTTGTCCTAACGCCAAGGTGTCCTGGGCTGTATGCGACTCACTGC  231
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          898  CCTGGGCTCTCCAGGCCCTGCTCTAATTAGGAGGTGAACCATGGACAACACAGCTGACTG  957

Qy          232  CCTTGGCTCTCCAGGCCCTGCTCTGATTAGGAGACATGAACCGTGGACACAGCTGACTG  291
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          232  CCTGGCTCTCCAGGCCCTGCTCTGATTAGGAGACATGAACCGTGGACACAGCTGACTG  291

Qy          958  CCATGTCTCTGGATTA-TGCTCACTGAAACTCACCCTTGCCCCTCAGGTC  1008
                 |||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          292  CCATGTCTCCGGATGACTGCTCACTGAGCTGAAAACTCCCTTGCCCCTCAGGTC  343
```

ORIGIN

```
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'),
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
```

Best Local Similarity   14.7%;   Score 148; DB 5; Length 735;
Matches 346; Conservative 56.4%; Pred. No. 1e-23;
        0; Mismatches 250; Indels 18; Gaps 3;

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Qy   143 AGGGGAAATGGCTGCGTTGGGTGGATGAAGCAGCGAGGGGCGGGGGTTGCAGCGAGC 202
             |||||||||||||  |||||||  ||||||||||  ||||||||||
Db     3 AGAGCAACCATTGCCTGGGATGCTCCAAGCGCCTGAATGACAACTGCAAGAAGC  62

Qy   203 TGCGCCTCCGAGTACGTAGGCGCAATCGCCTGGGCGGGGCCGGGGGGACCCGGGGAGCT 262
             ||||||||  |||||||||||||||||||  ||||||||  |||||||||||
Db    63 TGCGCTCCTCCTACAATCTCCATCTGCAACCGCGACATC------TCGCCCACCGAGCGCT 116

Qy   263 GCGTGCGCTCCCGTGCCCCGTGCCCCGCCGCTTCTTCTTCGTCGCGGGCCCTCCGGCGC 322
            |||||  ||||||||||||||||||||||||| | |||  |||||||||||||
Db   117 GCAACCGCGCCAAGTGCCACAAGGCCCTGGGCCGGGGGTGCCGGGGGTGCCCAGCGAGT 176

Qy   323 TCACGCACGCGCTGCTTCTTCTTGCGGATGCGAAGGCCCCGGCGGAGGGCGCGGGGCCC 382
             ||||||||||||||| ||||||||||||| |  |||||||||||||
Db   177 ACACCTACGCACGCATGCTCTTCTGCTCCTGCCAAGATCAGGCCGTGCCGCTGAGCGCGCCCGGC 236

Qy   383 AGACATTGCGCGCCGCCGGGCCGGGGCGTTCTCCGGCGCCCCCAGCGTGGGGCCCACCTTCCTGCGCCTGA 442
             |||||||||  ||||||||||||||||||||||||||||||||  |||||||||||  |
Db   383 AAACCATCCTGCCCAGCTG------CTCCTPATGAGGACAAGGAGGAAGCCCAAACTGCCCTGG 290

Qy   443 AGCCCTTGGACCGTGCGGAGGAAGCGCGGGTTCGG------CCCTGGTGCGCGTGTGAGGGCGAAAACCGGG 502
             ||||||||||||||||  |||||||  ||| ||||||||  |||||
Db   291 ACCTGGCGTGGGGTCGGGGGGACTGACCACCTGTGTCGGTGGTTCCGGCGTCCCGCGCCCGACTTCCATG 350

Qy   503 CCTCATGCGCTCCCGCGCCCGGCGTCGTCGCGGAGGAGGGGGGGCCGGGT 562
             |||||||  |||||||||||||||||||  ||||||||||
Db   351 CCAATTGTCGACGACGGGTCAACCAGTCGCCCTGCGGACACAATTACCAGGGCGT 410

Qy   563 GTCTCGCGGCGCCCACGCAGGCCCTTGTAGGCGATGGGTGTCACCCCAAACTACCTGGACAACG 622
             |||||||||||  ||||||||||||||||  |||||||||||  |||||||||  |||
Db   411 GTCTCGGGCGTCTTATCGTCGGCATGATTGGGGTTGACATGACCTAACTATGTGGACTCCA 470

Qy   623 TGAGCGCGGCGCGGTTGCG------CCCTGGTGCGCGTGTGAGGGCGAAAACCGGGCGCG 676
             |||||||  |  ||||||||||||  ||||||||||||||||||
Db   471 GCCCCACTGGCCATCCGTGGTGTGTCCCCCGTCGTCCGGGAGCTGTCTGCGGGCGAAACATGGAGG 530

Qy   677 AAGAGTGCGAAGCCTTCCCGCGGGAGCTTTTTTACAAGGAACCCTCGCTTGGGATGGGTGGCCATAC 736
            |||  |||||||||||||||||||||||||| | ||||||||||||||||||  |||||||||
Db   531 AGGAGTGTGAGAAGTTCCTCAGGGACTTCACCGAGAACCCATGCCTTCCGGAGAAACCGCCATCC 590

Qy   737 AAGCCTTTGACAGC 750
             ||||||||||
Db   591 AGGCCTTTGGCAAC 604
```

REFERENCE
AUTHORS Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
         Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
         Quackenbush,J. and Keele,J.W.

SOURCE
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
         1 (bases 1 to 633)
DEFINITION 554198 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION CB097266
VERSION CB097266.1 GI:2721458
KEYWORDS EST.
SOURCE Sus scrofa (pig)

LOCUS CB097266   633 bp   mRNA   linear   EST 27-JAN-2003
RESULT 14

FEATURES   Location/Qualifiers
   source   1..633
             /organism="Sus scrofa"
             /mol_type="mRNA"
             /db_xref="taxon:9823"
             /tissue_type="pooled"
             /clone_lib="MARC 2PIG"
             /lab_host="DH10B"
             /note="vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
             Library made from pooled tissue from testis, ovary,
             endometrium, hypothalamus, pituitary, and placenta."

ORIGIN

Best Local Similarity   14.3%;   Score 143.8; DB 6; Length 633;
Matches 203; Conservative 71.7%; Pred. No. 9.7e-23;
        0; Mismatches 77; Indels 3; Gaps 1;

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Qy   565 CTGGCGCGCCTACGCAGGGCCTTGTAGGCACCGTGGTCACCCCCAACTACCTGGACAACGTG 624
             |||||||||  ||||||||||||||||  |||||||||||||||||||||||||||||
Db     2 CTGAGCGCCTATGCCGCGCCCGCCTGCGTGGGGGACACCGCCGTCCCCGGCGAAGAGAGTGC 61

Qy   625 AGCGCGCGGCGCTTGCCCCCTGGTGCGGCCTCTGTGAGGCGCCAGGCGAGGCCGGAGAGTGC 684
             ||||||||||||||  ||||||||||||||||||||||||||  |||  ||||||||
Db    62 AGCGCGGCGGTGTGGCAACCTTGGCGGTGCGACTCGCGGAGAAACCGGCGTGAGGAGTGC 121

Qy   685 GAAGCCTTCCCGCAAGCGCTTTTTTACAAGGAGAACCCTCGCTTGGGATGGGTGGCCATACAAGCCTTT 744
             ||||||||||  ||||||||||||||  |||||||||||||||||||  |||||||||||||
Db   122 GAAGCCTTCCGGGGCGGCTTTTTACTAGGGAACCGGCGTGCCGCCATTCAGCCTTT 181

Qy   745 GACAGCTCGCAACATCAGTTCTCCAGGACCAGTGGACGACCCCTACCAGATGCTGGGCAG 804
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   182 GATGGTTGG----CCCCAATCCTACATGAACACCTGACCCCTCACCAGACTCTGAGCAC 238

Qy   805 GCCAAGGTGGGAGGGCTGAGTGGCCTGAGAAGAGAGATGGAGGGCAG 847
             ||||||||||||||||||||||||||||||||||||||  ||||
Db   239 CGCCTCCTCGAGGTGAGGTGCCACAGAGGAAGGTGAGCGCCAGCAG 281
```

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/,
         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

SOURCE
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
         1 (bases 1 to 822)
         Mus musculus
         Mus musculus (house mouse)
KEYWORDS EST.
VERSION CN539269.1 GI:46867425
ACCESSION CN539269
DEFINITION UI-M-HU0-cqt-i-24-0-UI.r1 NIH_BMAP_HU0 Mus musculus cDNA clone
         IMAGE:30667511 5', mRNA sequence.
LOCUS CN539269   822 bp   mRNA   linear   EST 29-APR-2004
RESULT 15

COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin University of Iowa
            cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousei.html
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.

FEATURES   Location/Qualifiers
        source   1..822
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30677511"
                     /tissue_type="whole eye"
                     /dev_stage="newborn(1, 5, 15 days)"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_HU0"
                     /note="Organ: Eye; Vector: pYX-Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel.First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is AATAATTACG. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP):'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH)."

ORIGIN
     Query Match   13.8%; Score 139.6; DB 7; Length 822;
     Best Local Similarity   55.6%; Pred. No. 9.4e-22;
     Matches 340; Conservative   0; Mismatches 254; Indels 18; Gaps 3;

Qy   143 AGGGGAAATCCGCTGCGTGGGAAGCAGCCGGAGCGGTGCACAGCAGCAGTGCCAGCAGC 202
         |||||| | |||| |||||||||| || |||||||| ||||||| ||| |||||||
Db   114 AGAGCAACCACTGCCTGGAGATCCCGCCAAGGGCCTGCAACCTGACACTGCACGAAAGC 173

Qy   203 TGCGGCTCCGAGTACGTGGCGCAAATGCCTGGGCCTGGGCGGGGGGACCCGGGAGCT 262
         ||||| |||| | |||||||| |||| ||| |||||||||||| ||| ||||
Db   174 TCCGGCTCTCCCTACAATCTCCATCTGCAAACCGGCGAGATCTCT------CCCACCGAAACGCT 227

Qy   263 GCGTGCGGCTCCCGCTCCGCGCCGGTGCCCTGCGCCGGCCTTCGTGCCCGGCGTCCGGCGC 322
         || ||||||| | ||||||| ||||| ||||||||||||||||||||||| ||||||
Db   228 GCAACCGCCGCAAGTGCCACAAGGCCCCTGCCCAGTTCTTCGACCGTGTGCCCAGCGAGT 287

Qy   323 TCACGGCACGCGGCCTGCTCTTTCGCGGATGCGAAGGCCCCGCCGTGGCCGGAGCGGGCGCC 382
         || ||||||||||| ||| |||||| ||||||||| |||||||| ||||| |||||| ||||
Db   288 ATACCTACCCGCATGCTTCTTCGCTCCTCGTGTCAGGACGGCAGGGACGGTGGCGGGC 347

Qy   383 AGACAATTCGGCGCCCCGCCGGCCGGTTCTCCGGCGCCACCTTCCTGCCTGA 442
         ||||| || ||||||| |||||| ||||| ||||| ||||||| ||||||||
Db   348 AAAACCAATCCTGCCCAGCTGTTCCTATGAGACAAAAGAGAAG-----CCCAATTGCTTGG 401

Qy   443 AGCCCTTGGACCGCTGCGAGGAAGCGCGCCGGTGCCCGGCGTCTTTTGCCTTCCAGG 502
         ||||| || ||||||| || ||||| ||| || |||||||||||||| ||||||
Db   402 ACCTGGGCAGGCTGTGTCGTACAGACCACTTGTGCCGGTCCCGCCTTGGCAGACTTCCACG 461

Qy   503 CCTCATGCGGCTCCCGCGGCGCCCCGACAGGCTGTCCGGAGGAGGGGGCCCGCGGT 562
         |||| ||||||| |||||| ||||||||| | ||||||||| ||||| |||||||||
Db   462 CCAACTGTCGAGCCCTCCTACCGGACAATCACCAGCTGCCTGCCGCACAACTACCAGGCAT 521

Qy   563 GTCTGCGCCGCCTACGGAGGCCTTGTGAGGCACCGTGGTTGATATGACACCGAACTAGTGGACTCCA 622
         ||||| ||| || ||| |||| ||||||| ||||| || ||| ||| | |||| |||||| ||||||
Db   522 GTCTGGGCTCCTATGCTGGCATGATGGGGTTTGATATGACACGGAACTAGTGTGGACTCCA 581

Qy   623 TGAGCGCGGCGCGGCCGTTGCG--------CCCTGGGGTGCGGCTGTGGAGGCCAGCGGGGAAAACCGGCGCG 676
         ||||| ||||||| || |||||| ||| |||||||| |||||| ||| |||||| ||||| |
Db   582 ACCCCACGGGCATCGGTGGGGTTCGGTGTTCCCGTTGCAATTGTCGTGGCGTGGGACACATGGAAG 641

Qy   677 AAGAGTGCGAACCCTTCCGCAGCTCTTTTACAAGGAACCCCTGCTTGGATGGGTTGCCATAC 736
         |||||| ||| ||||| ||||||| ||| ||||||| ||||||| ||| |||| ||| |
Db   642 AAGAGTGTGAGAAGTTCCTCAAGGACTTCACACGAGAAAACCCATGCCTCCGGAATGCCATTC 701

Qy   737 AAGCCCTTTGACA 748
         |||||||||||||
Db   702 AAGCCCTTTGGCA 713

Search completed: February 18, 2005, 03:55:33
Job time : 3973 secs

OM nucleic - nucleic search, using sw model

Run on:　　　　February 18, 2005, 01:31:13 ; Search time 2729 Seconds

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GenCore version 5.1.6

Title:　　　　　US-10-019-337E-7
Perfect score:　1008
Sequence:　　　1 ctggtaagcttaaggcaga..............aactccctgccctcagtc 1008

Scoring table: IDENTITY NUC
　　　　　　　Gapop 10.0 , Gapext 1.0

Searched:　　　5384158 seqs, 295248155 residues

Total number of hits satisfying chosen parameters:　　10768316

Post-processing: Minimum Match 0%
Maximum DB seq length: 200000000
Minimum DB seq length: 0

Maximum Match 100%
Listing first 45 summaries

Database :　　Published Applications NA:*

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4:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
5:	/cgn2_6/ptodata/2/pubpna/US07_PCT_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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10:	/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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21:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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SUMMARIES

Result No.	Score	Query Match	Length	% DB	Match ID	Description
1	299.6	29.7	995	10	US-09-866-050A-604	Sequence 604, App
2	299.6	29.7	995	14	US-10-152-661-604	Sequence 604, App
3	216.4	21.5	207433	17	US-10-277-216-5	Sequence 5, Appli
4	216.4	21.5	207433	17	US-10-126-022-5	Sequence 5, Appli
5	150.4	14.9	1392	9	US-09-388-316-2	Sequence 2, Appli
6	150.4	14.9	1392	15	US-10-357-822-2	Sequence 2, Appli
7	150.4	14.9	1490	18	US-10-673-007-10	Sequence 10, Appl
8	150.4	14.9	1995	15	US-09-388-316-15	Sequence 15, Appl
9	150.4	14.9	1995	15	US-10-357-822-15	Sequence 15, Appl
10	150.4	14.9	2600	9	US-10-357-822-1	Sequence 1, Appli
11	150.4	14.9	2600	15	US-10-357-822-1	Sequence 1, Appli

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

12	150.4	14.9	2906	18	US-10-723-860-3949	Sequence 3949, Ap
13	150.4	14.9	4232	18	US-10-872-161-35	Sequence 35, Appl
14	148.4	14.7	624	9	US-09-893-737-159	Sequence 159, App
15	139.4	13.8	4250	18	US-10-723-860-7856	Sequence 7856, Ap
16	135.2	13.4	2138	16	US-10-155-693-3	Sequence 3, Appli
17	135.2	13.4	2138	18	US-10-872-161-3	Sequence 3, Appli
18	135.2	13.4	3616	17	US-10-152-319A-1578	Sequence 1578, Ap
19	133.6	13.3	1407	15	US-10-357-822-20	Sequence 20, Appl
20	133.6	13.3	1927	16	US-10-155-693-9	Sequence 9, Appli
21	133.6	13.3	1927	16	US-10-155-693-40	Sequence 40, Appl
22	133.6	13.3	1927	18	US-10-872-161-9	Sequence 9, Appli
23	133.6	13.3	1927	18	US-10-872-161-48	Sequence 48, Appl
24	133.6	13.3	1929	16	US-10-155-693-11	Sequence 11, Appl
25	133.6	13.3	1929	16	US-10-155-693-41	Sequence 41, Appl
26	133.6	13.3	1929	18	US-10-872-161-11	Sequence 11, Appl
27	133.6	13.3	1929	18	US-10-872-161-49	Sequence 49, Appl
28	133.6	13.3	2378	14	US-10-033-350-1	Sequence 1, Appli
29	133.6	13.3	2560	18	US-10-393-590-4	Sequence 4, Appli
30	133.6	13.3	2560	16	US-10-393-590-5	Sequence 5, Appli
31	133.6	13.3	2560	16	US-10-393-590-39	Sequence 39, Appl
32	133.6	13.3	2560	16	US-10-393-590-40	Sequence 40, Appl
33	133.6	13.3	2560	16	US-10-393-567-4	Sequence 4, Appli
34	133.6	13.3	2560	16	US-10-393-567-5	Sequence 5, Appli
35	133.6	13.3	2560	16	US-10-393-567-39	Sequence 39, Appl
36	133.6	13.3	2560	16	US-10-393-567-40	Sequence 40, Appl
37	133.6	13.3	2560	16	US-10-394-087-4	Sequence 4, Appli
38	133.6	13.3	2560	16	US-10-394-087-5	Sequence 5, Appli
39	133.6	13.3	2560	16	US-10-394-087-39	Sequence 39, Appl
40	133.6	13.3	2560	16	US-10-394-087-40	Sequence 40, Appl
41	133.6	13.3	2560	17	US-10-172-118-1134	Sequence 1134, Ap
42	133.6	13.3	2560	17	US-10-295-027-83	Sequence 83, Appl
43	133.6	13.3	2560	17	US-10-058-270A-23	Sequence 23, Appl
44	133.6	13.3	2560	17	US-10-342-887-1134	Sequence 1134, Ap
45	133.6	13.3	2568	16	US-10-155-693-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-866-050A-604
; Sequence 604, Application US/09866050A
; Publication No. US20030040471A1
; Publication No. US200030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866,050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 604
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Mouse
US-09-866-050A-604

Query Match　　29.7%;　Score 299.6;　DB 10;　Length 995;
Best Local Similarity　77.8%;　Pred. No. 5.6e-78;
Matches　420;　Conservative　0;　Mismatches　49;　Indels　71;　Gaps　2;

Qy　　470 GCGGGTGCCGGAGCCCCCGGTCTTCTTTGGCTTCCAGGCCTCCCGGGGCTCC 529
　　　　　|| ||||||||||||||||||||||||||||||||||||||||||||||
Db　　17 GCGCGCGCCAGGCCCCGTCTTCCTTGGCCTTCCAGGCCTCATGCGCTCCCCC 76

Qy　　530 GCCACGGCGTTGTCCGGAGGAGGGGGGGGGGGGGCCGCGGTGTCTCGCGCGGCTACCGAGGGCTTGTAG 589
　　　　　||||||||||| |||||||||| |||||||| |||| |||||||||||| || |
Db

RESULT 2

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US-10-152-661-604
; Sequence 604, Application US/10152661
; Publication No. US20030022835A1
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT: Strachan, Lorna
;  APPLICANT: Sleeman, Matthew
;  APPLICANT: Onrust, Rene
;  APPLICANT: Murison, James G.
;  APPLICANT: Kumble, Krishanand D.
;  TITLE OF INVENTION: Compositions Isolated From Skin Cells
;  TITLE OF INVENTION:  and Methods for Their Use
;  FILE REFERENCE: 11000.101ic5
;  CURRENT APPLICATION NUMBER: US/10/152,661
;  CURRENT FILING DATE: 2002-05-20
;  PRIOR APPLICATION NUMBER: 09/866,050
;  PRIOR FILING DATE: 2001-05-24
;  PRIOR APPLICATION NUMBER: 60/221,232
;  PRIOR FILING DATE: 2000-07-25
;  PRIOR APPLICATION NUMBER: 60/206,650
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 09/312,283
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: PCT/NZ99/00051
;  PRIOR FILING DATE: 1999-04-29
;  PRIOR APPLICATION NUMBER: 09/188,930
;  PRIOR FILING DATE: 1998-11-09
;  PRIOR APPLICATION NUMBER: 09/069,726
;  PRIOR FILING DATE: 1998-04-29
;  NUMBER OF SEQ ID NOS: 725
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 604
;  LENGTH: 995
;  TYPE: DNA
;  ORGANISM: Mouse
US-10-152-661-604

  Query Match         29.7%;  Score 299.6;  DB 14;  Length 995;
  Best Local Similarity   77.8%;  Pred. No. 5.6e-78;
  Matches  420;  Conservative    0;  Mismatches   49;  Indels   71;  Gaps    2;
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Qy    317 AGGACCAGACTGCTGGGTGC------- 336
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Qy    337 -------------TGTTTCCCGCGGGGTGTTCCTGGGCTGTATGCA 366
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Qy    427 GCTGACTGCCCATGTCTCCCGATGACTGCTCACTGAGCTGAAAACTCCCTTGCCCTCAGGTC 486
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RESULT 3

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US-10-277-216-5/c
; Sequence 5, Application US/10277216
; Publication No. US20040002470A1
; GENERAL INFORMATION:
;  APPLICANT: KEITH, TIM
;  TITLE OF INVENTION: NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES,
;  TITLE OF INVENTION: OBESITY, AND INFLAMMATORY BOWEL DISEASE
;  FILE REFERENCE: 2976-4051
;  CURRENT APPLICATION NUMBER: US/10/277,216
;  CURRENT FILING DATE: 2002-10-17
;  PRIOR APPLICATION NUMBER: 10/126,022
;  PRIOR FILING DATE: 2002-04-19
;  PRIOR APPLICATION NUMBER: 09/834,597
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 09/548,797
;  PRIOR FILING DATE: 2000-04-13
;  NUMBER OF SEQ ID NOS: 420
;  SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
;  LENGTH: 207433
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-277-216-5

  Query Match         21.5%;  Score 216.4;  DB 17;  Length 207433;
  Best Local Similarity   77.7%;  Pred. No. 4e-53;
  Matches  278;  Conservative    0;  Mismatches   71;  Indels   71;  Gaps   11;
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Qy    530 GCGGACCGGCTGTCCGGAGGAGGGGGGCCCCCGGCCGGTGTCTGCGCGGCCTACCGCAGC 589
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Qy    590 GCACCGTGGTCACCCCCAACTACCTGGACAAACGTGAGCGCGGGCGGTTGGGCCCTGGGTGCG 649
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Qy    650 GCTGTGTGCGCGACCAGTGGAAAACGGGGCGGCGGAGAGTGGGAAGAGCCTTCCGCAAGCTCTTTACAA 709
Db    197 GCTGTGTGCGCGACCAGTGGAAAACGGGGCGGCGGAGAGTGGGAAGAGCCTTCCGCAAGCTCTTTACAA 256

Qy    710 GGAACCCCTGCTTGGATGGTTGCCATACAACGCCTTTGACAGCTCGCACCTACCTGGACAACGTAGC 769
Db    257 GGAACCCCTGCTTGGATGGTTGCCATACAACGCCTTTGACAGCTTGCAGCCATCAGTTCTGC 316

Qy    770 AGGACCAGTGGGAACCCCTACCAGAATGCTGGGCAGGCCAGGCCTGAGCTGCGAAGGCCT 829
Db    317 AGGACCAGACTGCTGGGTGC------- 336

Qy    337 -------------TGTTTCCCGCGGGGTGTTCCTGGGCTGTATGCA 366
Db    830 GAGAAGAGATGGAGGAGGCAGAAAACGGTCCCCGTTTTGTCTCCGATGGTCCATA 889

Qy    890 CTCACTGCCCTGGCTCTCCAGGCCCTCTAATTAGGAAGGTGAAACCATGGACAACACA 949

Qy    367 CTCACTGCCCTGGCTCTCGATTAGGAACACATGAAACCGTGGGACAGACACA 426

Qy    427 GCTGACTGCCCATGTCTCCCGATGACTGCTCACTGAGCTGAAAACTCCCTTGCCCTCAGGTC 486
Db    950 GCTGACTGCCCATGTCTCTCTGGATTA-TGCTCACTGAAACTGAAACTCCCTTGCCCTCAGGTC 1008
Db    427 GCTGACTGCCCATGTCTCCCGATGACTGCTCACTGAGCTGAAAACTCCCTTGCCCTCAGGTC 486

Qy    123 AGGGTGCAGCGACCAGCTCCACTGAGGGGAATCGCTGGGTGGTGGAAGACGCGAGGCGTGCACAGC 182
Db  86458 AGGGTCGGCGCGAGCTCGGTCGGCGAGGGAACCGATGTGTGGACGGGGCCAATGCGGGCGGCCGGCGG 86399

Qy    183 AGACGGAGCAGTGCCAGCAGCTGCGCTCCGAGTACGTGGCGGCAATGCCTGGGCGGGGCCGGGCCGGCGGG 242
Db  86398 GGACCGCGCGGTGCCAGCGGTTTGCGCTCCGAGTAGTGGGGCAGGTGCGCCTCGGGCC--- 86342
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OM nucleic - nucleic search, using sw model

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                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:             February 18, 2005, 01:19:23 ; Search time 278 Seconds
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Title:              US-10-019-337E-7
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Sequence:           1 ctggtaagcttaaggcaga.........aactcccttgccctcaggtc 1008
Scoring table:      IDENTITY NUC
                    Gapop 10.0 , Gapext 1.0
Searched:           1202784 seqs, 81818359 residues

Total number of hits satisfying chosen parameters:   2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :         Issued_Patents_NA:*
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                   6:/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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                            %
Result            Query
No.    Score   Match Length DB ID             Description
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  1    299.6    29.7  995    3  US-09-724-864-35   Sequence 35, Appli
  2    150.4    14.9  1392   3  US-08-957-063-2    Sequence 2, Appli
  3    150.4    14.9  1392   3  US-09-245-041-5    Sequence 2, Appli
  4    150.4    14.9  1392   3  US-08-802-805D-2   Sequence 2, Appli
  5    150.4    14.9  1392   4  US-09-388-316C-2   Sequence 2, Appli
  6    150.4    14.9  1490   4  US-08-861-990-10   Sequence 10, Appl
  7    150.4    14.9  1888   4  US-09-187-906-12   Sequence 12, Appl
  8    150.4    14.9  1995   3  US-08-957-063-15   Sequence 15, Appl
  9    150.4    14.9  1995   3  US-09-487-685-15   Sequence 15, Appl
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ALIGNMENTS

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US-09-724-864-35
Sequence 35, Application US/0972486 4
; Patent No. 6380362
; GENERAL INFORMATION:
;  APPLICANT:  Watson,
;  APPLICANT:  Murison, James G
;  APPLICANT:  Watson, James D
;  TITLE OF INVENTION:  Polynucleotides, polypeptides expressed
;  TITLE OF INVENTION:  by the polynucleotides and methods for their use.
;  FILE REFERENCE:  11000.1050U1
;  CURRENT APPLICATION NUMBER:  US/09/724,864
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER:  U.S. No. 6380362 60/171,678
;  PRIOR FILING DATE:  1999-12-23
;  NUMBER OF SEQ ID NOS:  72
;  SOFTWARE:  FastSEQ for Windows Version 4.0
;  SEQ ID NO 35
;    LENGTH:  995
;    TYPE:  DNA
;    ORGANISM:  Mouse
US-09-724-864-35

  Query Match          29.7%;  Score 299.6;  DB 3;  Length 995;
  Best Local Similarity   77.8%;  Pred. No. 5.6e-63;
  Matches  420;  Conservative  0;  Mismatches  49;  Indels  71;  Gaps  2;
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Qy   950 GCTGACTGCCCATGTCTTCTGGATTA-TGCTCACTGAAACTGAAACTCCCCTTGCCCTCAGGTC 1008
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RESULT 2
US-08-957-063-2
; Sequence 2, Application US/0895706
; Patent No. 6025157
GENERAL INFORMATION:
; APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes
TITLE OF INVENTION: Neurturin Receptor
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,063
FILING DATE: 24-Oct-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/871
FILING DATE: 9-Jun-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 913
FILING DATE: 18-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1086P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-957-063-2

Query Match   14.9%;   Score 150.4;   DB 3;   Length 1392;
Best Local Similarity   56.0%;   Pred. No. 7e-27;
Matches   355;   Conservative   0;   Mismatches 261;   Indels 18;   Gaps   3;

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Qy   243 CTGGCGGGGGAGACCCGGGAGCTGGCGGTCGGTCGCGCTCCCGCTTGCCGCGCGGCGCCGGGGCGCTCTT 302
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Qy   423 GGCGCGCACGTTCCTGCCTGAAAGCCCTTGGACGGCGTGCGAGGAAGCCGGCGGGGGCC 482
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Db   918 ACCTAACTATGTGGACTCCAGCCCCACTGGCCATCGGTGGTGTCCCCCGTGGTGCAGCTGTCG 977

Qy   657 GGCCAGCGGAGAAACCCGCGCGCCGCAAAGAGTGCGAAGCCCTTCCGGCAAGCTTTTCAGAAGGAGAAACC 716
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Qy   717 CTGCTTGGATTGGTGCCATACAAGCCTTTGACAGC 750
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RESULT 3
US-09-487-685-2
; Sequence 2, Application US/0948768
; Patent No. 6342348
GENERAL INFORMATION:
; APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes
TITLE OF INVENTION: Neurturin Receptor
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/487,685
FILING DATE: 19-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/957,063
FILING DATE: <Unknown>
APPLICATION NUMBER: 913
FILING DATE: 18-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1086P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs